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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 02068652-A 47 06-SEP-2002;
Location/Qualifiers
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AX921054

    .2071
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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AX481748 Sequence
BC006156 Homo sapi
BC039961 Homo sapi
BC08325 Homo sapi
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(c) 1993 - 2004 Compugen Ltd.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943(
Web site: (Dickson, Mark) med@paxil.stanford.edu
Contact: (Dickson, Mark) med@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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This clone was selected for full length sequencing because it passed the following selection criteria: Excellent library of origin.
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99.9%; Pred. No. 2.3e-227;
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/do_type="mRNA"

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/clone="INE" MIH MGC_95"

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/note="Wector: pBluescript"
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CCGGCCTGCTGCTGCTGTTCATCTGTAGCTTCATGGTGGCTGCCCCCATCTTCGGCT   420	TGGGCAGTGGCCTGGGCTGAAGCGGGCGGGGCGGGGGCGGGGGCGGGGGCGGGGGCGGGGCCGGGG	1081   CGGGGCAGGAGCCAGCGCGCCCAGAGACCCAGCGGGCGACCCACTGGTT   1140   CGGGGGCAGCCACCGGCGCGCGCCCACTGGTT   1141   CGGGGGCCATGCTCGCCATCTCATCATCGCCACTGCTGCATGTTTCTAACT   1285   1141   GTGCCGTGGCCATGCTCGCCATCTTCGTCGCTGCCTGCCAGA   1285   1141   GTGCCGTGGCATGCTGCCATCTTCGTCGCTGCCTGCCAGA   1200   1286   GCAGCATCGTGGCTTCTCTTCGTCGCTGCTGCTGCCAGA   1200   1246   GCAGCATCGTAGCTTGCTTTTCTTAACT   1345   GCAGCATCGTGCAGCCTTTTTTTTTTTTTTTTTTTTTTT
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0y         1441         GACGCCGGGAGCCCCTACCTCATTGGCTTTATCTCAGACCTGATCCGCCAGAGCACTAAG         1500           1624         GACGCCGGGAGCCCCTACCTCATTGGCTTTATCTCAGACCTGATCCGCCAGAGCACTAAG         1683           0b         1624         GACGCCGGGAGTTCCTGAGCTTGGGCTACGCCTCATGCTCTGCCCTTTCGTC         1560           0y         1611         1111 <td>AX179748 AX179748 LOCUS LOCUS AX179748 AX179748</td> <td>  0   0   0   0   0   0   0   0   0   0</td>	AX179748 AX179748 LOCUS LOCUS AX179748	0   0   0   0   0   0   0   0   0   0

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HLLGDRASSPYLIGFISDLIRGSTKDSPLWBFLSLGYALMLCPFVVVLGGMFFLATALF
FLSDRAKAEQQVNQLVMPPASVKV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGGGCTGGAGGTAGCGCTTGCTGCGGGGCGCGCGGGGTGTTGGGGGGCGCTGGAGTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GCCGCGGGCGATGAGGTGCAGACGCTGTCGGGCAGCGTAAGGCGGGCCCCGACCGGACCC
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85.6%; Pred. No. 4.3e-186;
ive 0; Mismatches 252; Indels
                             tumor.
/clone="IMAGE:3154539"
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/clone lib="NCI CGAP_Mam3"
/lab_host="DH10E"
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                                                                                                                                                                                                                                                                                                                                                          protein_id="AAH11467.1"
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                                                                                                                                                                    /gene="BC011467"
                                                                                                                                                                                                                                                                                     /gene="BC011467"
/codon_start=3
                           /tissue_ty
months old
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Kausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Mallahy, S.J., Boakk, S.A., McEwan, P.J.,

McKernan, K.J., Mallahy, S.J., Boakk, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Retteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                          3273 bp mRNA linear ROD 16-SEP-2003
ce BC011467, mRNA (cDNA clone
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ph.D.
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 23 Row: b Column: 10.
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                   Chu-Xia Deng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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                                                                                                                                                                                                              Mus musculus cDNA sequence B(
IMAGE:3154539), partial cds.
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                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                            BC011467
BC011467.1 GI:15079261
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                                                                                                                                       RESULT 4
BC011467
LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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AUTHORS
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MEDLINE
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COMMENT
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17-AUG-1999 US 60/149639,23-SEP-1999 US 60/155686 PR 01-0CT-1999 US 60/157247,29-NOV-1999 US 60/167823 PR 29-NOV-1999 US 60/167822,15-FEB-2000 US 60/167823 PR 60/167822,15-FEB-2000 US 60/167821 PI DARIO VALENZUELA,OLIVE YUAN HEIDI HOFFMAN, JEFF HALL, PETER PI RAPIEJKO PC C12N15/09,A61K38/00,A61P3/10,A61P2/14,A61P11/00,A61P11/06, PC A61P31/04,A61P25/14,A61P27/02,A61P29/00,A61P31/04,A61P31/12,PC A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12,A61P31/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGCAGAAGACGCGAGCAGACGTGCAACAGCCCGCCCTGTGGGGCCAAGGACACACTGT
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Location/Qualifiers
1. 2342
| "Craganism="Homo sapiens" | mol type="genomic DNA" | db_xref="taxon:9606"
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.larity 99.6%; Pred. No. 7.6e-91;
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I. (bases 1 to 2142)
Valenzuela, D., Yuan, O., Hoffman, H., Hall, J. and Rapiejko, P. Secreted proteins and polynucleotides encoding them ALPAGENE INC
ALPAGENE INC
S Homo sapiens (human)
PN JP 2002536973-A/10
PR 19-FEB-2000 JP 2000599860
PR 19-FEB-1999 US 60/120680,23-APR-1999 US 09/298733 PR
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JP 2002536973-A/10.
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1836 bp mRNA linear PRI 21-OCT-2003
Homo sepiens spinster-like, mRNA (cDNA clone IMAGE:3627317),
partial cds.
BC006156.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human sugar transporter proteins, potassium channel proteins,
human sugar transporter proteins and methods of use thereof
phospholipid transporter proteins and methods of use thereof
batent: WO 02055701-A 6 18-JUL-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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    1587
/note="unnamed protein product"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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[Carbohydrate transport and metabolism]"
/db_xref="CDD:COG2814"
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/gene="SPINL"
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Klausherg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausherg, R. L., Feingold, E. A., Grouse, L. H., Schenfer, C. M., Schuler, G. D.,
Klausner, R. L., Collins, P. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Altschul, S. P., Zeeberg, B., Buetow, K. H., Scheefer, C. F., Bat, N. K.,
Hopkins, R. F., Jordan, H., Mooret, T. Mark, S. L., Wang, J., Haieh, F.,
Distchenko, L., Marulana, K., Parmer, A.A., Rubin, G. M., Hong, L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Moreman, K. J., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
Morkernan, K. J., Male, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Vilalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Dickson, M. C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R. M.,
Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
Schein, J. S., Marny, D. M., A., Marny, D. M., Sodergrein, J. Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
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Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
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/product="SPINL protein"
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Tissue Procurement: ATCC
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Libburg Thousement and CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc.mgc@nhgri.nih.gov/

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
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TLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGDAGSPYLIGLISDRLRRNWP
PSFLSEFRALQPSLMLCAFVGALGGAAFLGTAIFIEADRRRAQLHVQGLLHEAGSTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01.NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences hum. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257
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/mol_type="mRNA"
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Conteact: MGC halp desk
Email: cgapbs.r@mail.nih.gov
Email: cgapbs.r@mail.nih.gov
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1. (bases 1 to 2017)

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Mooret, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Halton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
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1059 AGTTGTGCA---GAAGACAGCAGAGACGTGCAACAGCCCGCCCTGTGGGGCCAAGGACAG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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'db xref="CDD:COG2814"
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Rakhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Legaspl,R.,
Hansen,N., Mo.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspl,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="LocusID:83985"
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ALRVTPGLGVVPVLLLFLVVREPPRGAVERHSDLPPLNPTSWWADLRALARNPSFVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLGFTAVAFVTGSLALWAPAFILRSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGV
GYGGLGVELSRRLRHSNPRAPDLVGYTGLLGGSAPFLFLGAGAGGSIVAYTFFISTG
TLLSRNWMAIVADILLYVVIPPRAFRARAFQIVLSHLLGDAGSPYLIGLISDRLRRWP
PSFLSEFRALQFSLMLCAFVGALGGAAFLGTAIFIEADRRRAQLHVGGLLHEAGSTDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRMK Plate: 140 Row: m Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Sugar tr; Region: Sugar (and other) transporter"
/db_xref="CDD:pfam00083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerreceaearcaearcireaacareegeaearaereregeereregeereareeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Skin, melanotic melanoma."
/done_lib="NH MGC 72"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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larity 64.3%; Pred. No. 3e-72;
Conservative 0; Mismatches 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:70841 IMAGE:6161778"
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/gene="SPINL"
/db_xref="LocusID:83985"
123. 1709
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/protein_id="AAH65235.1"
/db_xref="GI:40807118"
/db_xref="LocusID:83985"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .2049
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Matches 879; Conserv
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/ LEAR 1 at 10m = "MAGSDTAPPLSQADDPDDGPVPCTPGLPGSTGNPKSEEPEVPDQ
BGLQRITGLSPGRSALIVAVLCYINLLNYMRRFTVAGVLPDIEQFFRIGDSSSGLIQT
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PSFLSEFRALQFSLMLCAFVGAAFLGTAIFTEADRRRAQLHVQGLLHEAGSTDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 CGCCATCCTCAGCTTGGGCAACGTGCTCAACTACCTGGACAGGTACACCGTGGCAGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.2%; Score 563.8; DB 9; Length 64.3%; Pred. No. 3e-72; ive 0; Mismatches 482; Indels
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/clone="MGC:15767 IMAGE:3501826"
/tissue_type="Brain, neuroblastoma"
/clone_lb="NIH MGC_19"
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|db_xref="G1:14249892"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="LocusID:83985"
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/db_xref="LocusID:83985"
                                    'organism="Homo sapiens"
                                                                                                                                                                                                                                       'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIVVPQRGRSTRVPVASVLI"
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Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Hsich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
D. Argon, B. 1977931
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                       2050 bp mRNA linear PRI 29-JUN-2004
Homo sapiens spinster-like, mRNA (cDNA clone MGC:15767
IMAGE:3501826), complete cds.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (125-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
CGCGCTCATGCTCTGCCCTTTCGTCGTGGTCCTGGGCGATGTTCTTCCTCGCCACTGC
                                                                                                                  GCTCTTCTTCGTCAGCGACCGCCCAGGGCTGAGCAGCACCTGGGGG 1642
                                                                                                                                                                  1568 CATCTTCATTGAGGCCGACCGCGGGGGCACAGCTGCACGTGCAGG 1614
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                    BC008325.1 GI:14249891
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/translation="MAGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEEBEVPDD
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RIVVPQRGRSTRVPVASVLI"
             Mol. Cell. Biol. 21 (11), 3775-3788 (2001)
21238517
2 (bases 1 to 2165)
2 (bases 1 to 2265)
Direct Submission
Submitted (08-DEC-1999) Pioneering Research, Mitsubishi Kasei Institute of Life Sciences, 11, Minamiooya, Machida, Tokyo 194-8511, Japan
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/note="similar to Drosophila spinster protein; SPINI"
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/product="spinster-like protein"
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Pred. No. 3e-72;
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Shimoda, Y., Fujitani, K., Kurihara, J., Ragan, J., Usui-Aoki, K.,
Shimoda, L., Lukacsovich, T., Suzuki, K., Sezaki, M., Sano, Y., Ueda, R.,
Autano, W., Kaneda, M., Umeda, M. and Yamamoto, D.
Mutations in the novel membrane protein spinster interfere with
programmed cell death and cause neural degeneration in Drosophila
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GACACCGGGTCTAGGAGTGGTGGCCGTTCTGCTGCTTCCTGGTAGTGCGGGAGCCGCC
                                                AAGGGGTCATGCCGACCAGCTCGGGGA---CCAGGTCAAGGCCCGGACCTCATGGCTCCG
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Homo sapiens spinster-like protein mRNA, complete cds.
AP212371
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VERSION KEYWORDS SOURCE

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FEATURES Location/Qualifiers  source 12230 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /db_xref="taxon:9606" /db_xref="unnamed protein product" /codom start=1 /codom start=1	/db_xref="G1:22316581" /db_xref="G1:22316581" /translation="WAGSDTAPFLSQADDPDGPVPGTPGLPGSTGNPKSEEPEVPDQ EGLQRITGLSPGRSALIVAVLCYINLLNYMDRFTVAGVLPDIEQFFNIGDSSSGLIQT SGLORITGLSPGRSALIVAVLCYINLLNYMGRSTVAGVLPDIEQFFNIGDSSSGLIQT VPTSSYMVLAPVFGYLLGDRYNRKYLWGGGTAFWSLVTLGSSTIPGEHWLLLLTRGLV GVGBASYSTIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKDMAGDWHW ALRYTPGGLGVWAVLLLFLVVREPPRGAVERHSDLPPLNPTSWADLRALARNPSFVLS SLGFTAVAFVTGGLALMAPPAFLLRSRVVLGSTPPCLPGDSCSSSDSLIFGLITCLTGV LGYGLGVELSRRLHSRNPRADPLVGATGLLGSTPGLSGSIVATYIFFIGE TLLSMNWAIVADILLYVVIPTRRSTARARQIVLSHLLGDAGSPYLIGLISDRLRRNWP	ORIGIN  ORIGIN  Query Match  Best Local Similarity 64.38; Pred. No. 3e-72;  Matches 879; Conservative 0; Mismatches 482; Indels 6; Gaps 2;	0y 282 GGGCCCGGCGCTCAGCAGCCCAAACCGGCCGGGGGGGGGG	Qy         402 CCTTCTGGACATCCAGCAGCACTTTGGGGCGCCGGCCGGC	Qy         522         CAACAGGAAGGTGATTCTCAGCTGGCAGCTTTTCTTCTGGTCGGCGTCACCTTCTCCAG         581           Db         741         CAATCGGAAGTATCTCATGTGCGGGGGCATTGCCTTCTGGTCCTGGTGACACTGGGGGT         800           Qy         582         CTCCTTCATTCCCCAGCAGTACTTCTGGCTGGTCCTGTCCCGGGGGCTGGTGGGGAT         641           Db         801         ATCCTTCATTCCCCGGAGGCATTTTCTGGCTGCTCCTCCTGGCGGGCTTGGTGGGGGT         860	Qy         642 CGGGGAGGCCAGCTACTCCACCATCGCCCCACTATCATTGACCACTCTTCACCAGAA 701	Db   921   CCGCGGGGCGGGTGCTCTCTGTTTTGCTTTGCGTGGGTGTGTTTTTT
	Db         1110 AdATCTGAGGGCCCTGGGCATGTACGTCCTGTCTTCCTGGGCTTCACTGGCTTCACTGGCTTCACTGGCTTCACTGGCTTCACTGGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGCTTCCTGTTCTTC	1116 CCTCATCTTTGGGGCCATCACCTGCTTTACGGGATTTCTGGGCGTGGTCACGGGGGCAGG 117  1290 TCTCATCTTTGGACTCATCACCTGCCTGACGGAGTCTGGGTGGTGGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTG	140 129 146 135	1356 TGCAGACATCCTCATGTACGTGGTCATCCCCACGCGCGCG	1590 GATCGTGCTGTCCCACCTGGTGATGCTGGGAGCCCCTACCTCATTGGCCTGATCT 164  1476 AGACCTGATCGCCAGAGCACTAAGGACTCCCGGCTCTGGGAGTTCCTGAGCCTGGTA 153  1650 TGACCGCCTGCGCGGGAACTGGCCCCCCTCCTTCTTGTCCGAGTTCCGGGCTCTGCAGTT 170  1536 CGCGTCATGCCTTCGTCGTGGTCCTGGGGATTCTTCCTCGCCAGTT 170  1536 CGCGTCATGCCTTTCGTCGTGGTCCTGGGGCATGTTCTTCCTCGCCAGTT 170	DD 1710 CTCGCTCATGCTCTGCGCGTTTGTGGGGGGCGCGCGGGGGCGTTCCTGGGGCACCGC 1769  Qy 1596 GCTCTTCTTCGTCAGCGACCGCCAGGGCTGAGCAGCACCTGGGGG 1642	AX481746  AX481746  AX481746  LOCUS  Sequence 4 from Patent W002055701.  AX61746  AX

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M RUBEN, CRAIG A ROSEN, CARRIE L FISCHER, DANIEL R SOPPET, PI
KENNETH C CARTER DANIEL P BEDNARIK, GREGORY
A ENDRESS, GUO LIANG
PI YU, JIAN NI,
PI PING FENG, PAUL E YOUNG, JOHN M GREENE, ANN
M FERRIELS, ROXANNE DUAN,
PI JING SHAN HU, KIMBERLY A FLORENCE, HENRIK
S OLSEN, REINHARD EBNER,
PI LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI
I, YI LI, ZHIZHEN ZENG,
PI HLA KYAW
PI C 122NIS/12, C12NS/10, C12NI/21, C07KI4/47, C07KI6/18, C12QI/68, PC
GOIN33/50,
PC GOIN33/50,
PC GOIN33/51, Cnoar;
CC Strandedness: Double;
CC Strandedness: Double;
FH Key
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Cl2N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68,
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Pred. No. 3.3e-69;
1; Mismatches 478;
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    .2201
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Ruben.S.M., Portion.

Ruben.S.M., Fartie, A.M., Vis, C.L., Soppet, D.R., Carter, K.C., Bednarik, D.P., Endress, G.A., Yu, G.L., N.J., Feng, P., Young, P.B., Greene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A., Lafleur, D.W., Li, Y., Enga, Z. and Kyaw, H.

Bednarik, D.P., Endress, G.A., Yu, G.L., N.J., Feng, P., Young, P.B., Gleene, J.M., Li, Y., Engy, Z. and Kyaw, H.

Lafleur, D.W., Li, Y., Zang, Z. and Kyaw, H.

Batent: JP 2002510192-A, 239 02-APR-2002;
PN JP 2002510192-A, 239 02-APR-2002;
PN JP 2002510192-A, 239
PD 02-APR-2002
PP 06-MAR-1999 JP 1998538883
PR 07-MAR-1997 US 60/040162, 07-MAR-1997 US 60/040161 PR 60/040526;
07-MAR-1997 US 60/040526, 07-MAR-1997 US 60/040538 PI STEVEN 11-APR-1997 US 60/040336, 07-MAR-1997 US 60/04036, 07-MAR
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Query Match 26.2%; Score 542.8; DB 6; Length 2201; Best Local Similarity 64.3%; Pred. No. 3.3e-69; Matches 877; Conservative 1; Mismatches 478; Indels 8; Gaps 4; Qy 285 CCCGGGGCTCAGCAACCGGCCAACCTGGGCGGGGGGGGGG		Db 476 GGTGCTGTGTTATTTTTTTTTTTTTTTTTTTTTTTTTTT	Db 536 TCCCGCACATCCAGCAGCCGTCGGGGCAGTAGCTCTGGGCTCATCCAGACCGT 595  Qy 465 GTTCATCTGTAGCTGGTGGCGCCCCCATCTGGGCTACCTGGGCGACCGCTTCAA 524	Db 596 dricarcradriacardriagearcraderarraderarraderacardacada 655  Qy 525 CAGGAAGGTGATTCTAGCTGGGGGATTTTCTTCTGGTGGCCGTCACCTTCCAGCTC 584	656 TCGGAAGTATCTCATGTGCGGGGGCATTGCCTTCTGGTCCTGGTGACTGGGGCTCATC 585 CTTCATTCCCCAGGAGACTTCTGGCTGCTGCTGCTGCTGCGGGGGTTGGTGGGGAATCGG	716 CTTCATCCCGGAGGATTCTGGCTGCTCCTCCTGACCCGGGGCCTGGTGGGGGTCGG 645 GGAGGCCAGCTACCCCCCCCACTATCATTGGCGACTCTTCACCAAGAACAC	Db 776 GGAGGCCAGTTATTCCACCATCGCGCCCACTCTCATTGCCGACCTCTTGTGGCCGACCA 835  Qy 705 GCGTACGCTCATGCTGTCCGTCTTCTACTTCGCCATCGCCAGGCAGTCGCCTGGGCTA 764	Db 836 GCGGAC-CGGATGCTCAGCATTTTTTTTTTTTTTTTTTTT	Db 895 CATTGCAGGCTCCAAAGTGAAGGATATGGCTGGAGACTGGGCTCTGAGGGTGAC 954  Qy 825 CCCTGTCCTGGGCATGATCACAGGAACACTCATCCTCATTCTGGTCCACTAAAAA 884	955	Db   1015   GGGGCCGCGCCCCCCCCCCCCCCCCCCCCCCCCCCC
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Search completed: October 23, 2004, 11:01:11 Job time : 8813 8ecs

Adh73962 Human sec

Aav59740 Human sec Aav59741 Human sec Abs7373 Human sec Abs7373 Human sec Ads73961 CDNA enco Adv29587 Human sec Adv37574 Human sec Adv37574 Human sec Adv373674 Human sec Adv373804 Human sec Adv373804 Human sec Adv373804 Human sec Adv3726 Human tra Adv37276 Human tra Adv37276 Human adu Adv37896 Human CGD Adv37890 Human CGD Adv3789 Human CGD

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Run on:

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Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic; hypotensive; attiatretriosclerotic; anorectic; gene therapy; NOV19; spinster-like protein; chromosome 17; gene; ds; SNP; single nucleotide polymorphism.
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28-FEB-2001; 2001US-0272404P.
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02-MAR-2001; 2001US-0272414P.
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30-MAR-2001; 2001US-0278660P.
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Ad74263 Human 464
Ad6127958 Human 464
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12-APR-2001; 2001US-0283443P.
23-APR-2001; 2001US-0286754P.
24-APR-2001; 2001US-0286096P.
03-WAY-2001; 2001US-0288353P.
17-MAY-2001; 2001US-0294834P.
20-UIN-2001; 2001US-0294834P.
20-UIN-2001; 2001US-0299845P.
21-UIN-2001; 2001US-0299845P.
13-AUG-2001; 2001US-031931P.
16-AUG-2001; 2001US-0313280P.
29-AUG-2001; 2001US-0313280P.
29-AUG-2001; 2001US-031380P.
29-AUG-2001; 2001US-031381P.
17-SEP-2001; 2001US-031281P.
25-FEB-2002; 2001US-0322818P.
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                                                                                                                                                    1681 CCGGGCCCGGGCACTGCTCTGGCACATCGTGTGGGGGGGCCCAGCTGACCGGAGGTGCTG
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/product= "Human TRICH-9 protein"
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WO200146258-A2

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The present sequence is transporter and ion channel-9 (TRICH-9) cDNA.

TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease, anticolar disorders including Alzheimer's pick's disease, mental disorder, muscle stroke, cerebral neoplasms, Pick's disease, mental disorder, including cardiomyopathy, myocarditis, polymyositis, andit respiratory distress syndrome (ARDS), allorgies, including ALDS, adult respiratory distress syndrome (ARDS), allorgies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracte, infertility, pulmonary arter, stenosis, Grave's disease, Cushing's disease, Addison's disease, calcaractes, infertility, bulmonary arcer, stenosis, date will be some syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, ingene therapy and in diagnostic
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איר. Gandhi AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing transport, neurological, muscle and immunological disorders.
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                                                                                                                                                                                                                                                                                                        DAM, Yang J, Reddy
Nguyen DB, Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3179 BP; 562 A; 1036 C; 962 G; 619 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human transporter and ion channel proteins useful for
                                                                                                                                                                                                                                                                                                        Lu DAM,
H, Nguye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 146-147; 160pp; English.
                                                                                                                                                                                                                                                                                                        N, Au-Young J,
Azimzai Y, Yue
2000US-0176083P.
2000US-0177332P.
2000US-0178572P.
2000US-0179758P.
                                                                                                                                                       2000US-0181625P
                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                Baughn MR, Burford N,
Lal P, Hillman JL, Az
Tang YT, Khan FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-418042/44.
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Matches 1549;
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                                                                                                                          GCCTGGGCTACGCGCTCATGCTCTGCCCTTTCGTCGTGGTCCTGGGCGGCGATGTTCTTCC
                                               GCTTTATCTCAGACCTGATCCGCCAGAGCACTAAGGACTCCCCGGTTCTGGGAGTTCCTGA
                     GCTTTATCTCAGACCTGATCCGCCAGAGCACTAAGGACTCCCCGCTCTGGGAGTTCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding sequence (useful for identifying genetic disorders) #481
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                                                                                                                                                                                 TCGCCACTGCGCTCTTCTTCGTCAGCGACCGCCCAGGGCCTGAGCAGCACCTG 1638
                                                                                                                                                                                                       novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides, useful for expressing recombinant proteins fanalysis, characterization or therapeutic use, or as markers for in which the corresponding protein is preferentially expressed.
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vu P, Drmanac RT,
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Pred. No. 2.3e-161;
0; Mismatches 1;
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hrman T, Weng G, Zhou P,
R, Xu C, Boyle BJ;
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                                                                                                  GCCTGGGCTACGCGCTCATGCTCTGCCT
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-036591P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-037261SP.
22-APR-2002; 2002US-0012858
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Ghosh M, Xue AJ, Wehrman T,
Ma Y, Wang D, Chen R, Xu C,
                                                                                                                                                                                                                                                                                                                               ADE07415 standard; DNA; 1250
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Best Local Similarity 99.9%
Matches 934; Conservative.
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P-PSDB; ADE08326.
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GCGGGGGCAAGCCGCCGCCATCCTCAGCTTGGGCAACGTGCTCAACTACCTGGACAGGT
                                                                      ACACCETGEGEGEGETCTTCTGGACATCCAGCACTTTGGGGTCAAGGACCGAGGCG
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secreted protein coding sequence SEQ ID NO: 19.
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17-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for a human secreted protein. It was isolated from an adult pancreas cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
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Human, secreted protein; cytokine; cell proliferation;
nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New secreted proteins and polynucleotides encoding them, derived from Homosapiens, useful for therapy, diagnosis, well as nutritional sources or supplements.
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                                                                                                                                  Location/Qualifiers
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99US-00298733.
99US-0149639P.
99US-0155686P.
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99US-0167823P.
2000US-0182711P.
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P-PSDB; AAB23610.
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immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypoptide or polynucleotide strength in gene therapy. A composition containing a polypoptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system disease, such as lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and contains, assays for receptor activity, arthritis and inflammation, leukaemias and contains, and contains and thrombolytic activity arthritis and inflammation, leukaemias and contains.
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                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1024 GGCATGTGGATCCCGCTCTACCTGCACCGCCCAAGTTGTGCAGAAGACAGCAGAGACG
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                                                                                                                                                            vel nucleic acids and polypeptides, useful for treating disorders central nervous system injuries.
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                                                                       Ren F,
Zhang,
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Yang Y,
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                                                                    Ma Y,
Xue AJ,
                                                                                                                                                                                                   Claim 1; SEQ ID NO 1532; 10078pp; English.
                                                                    Chen R,
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                                                               Liu C, Asundi V, Chen
Wang Z, Wehrman T, Xu C
Goodrich R, Drmanac RT;
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             29-NOV-2000; 2000US-00727344
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                                                                                                                    WPI; 2001-442253/47.
P-PSDB; AAM40173.
                                     HYSEO INC.
                                                              Tang YT,
Wang J,
Zhou P,
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                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                        CATCCTCATGTACGTGGTCATCCCCACGCGCGCGCCACTGCCGTGGCCTTGCAGAGCTT
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26-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-005312.
03-AUG-2000; 2000US-0055315.
14-SEP-2000; 2000US-0055315.
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                                                                                                                                                                                                                                                 1024 GGCATGTGGATCCCGCTCTACCTGCACCGCGCCCAAGTTGTGCAGAAGACAGCAGAGACG
                                                                                                                                                                                                                                                                                                               GGCATGTGGATCCCGCTCTACCTGCACCGCCCCTTGTTGTGCATAAGACAGCAGAGACG
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                                                                                                                            DB 4;
                                                                                                                        Score 603.8; DB 4;
Pred. No. 4.3e-101;
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part of the printed specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
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, Zhao C
                          GICCTGGGCGGCATGITCITCCTCGCCACTGCGCTCTTCGTCAGCGACCGCGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's Parkinson's disease; hacense; hacensetatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic
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Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic; immunosuppressant;
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-0059317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653180.
14-SEP-2000; 2000US-00663191.
19-OCT-2000; 2000US-00663191.
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                                                                                                                                               1624 GCTGAGCAGCACCTG 1638
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Goodrich R,
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P-PSDB; AAM41959.
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Wang J,
Zhou P,
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New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                  /*tag= a
/product= "46455 transporter protein"
                      Location/Qualifiers
                                                                                                                                                                                                  Claim 1; Fig 8; 364pp; English.
                                                                                           15-DEC-2000; 2000US-0256240P.
18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
                                                                              17-DEC-2001; 2001WO-US049060
                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                              WPI; 2002-590672/63.
                                                                                                                                                     P-PSDB; ABP52155
                                                    WO200255701-A2
       sapiens
                                                                                                                                   Curtie RAJ;
                                                                                                                                                                                       disorders.
       Homo
                    Key
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The present sequence encodes the human 46455 protein, which is a member of the transporter family. The transporter family proteins (I) of the present invention have anorectic, antidiabetic, anti-Parkinsonian, cardiovascular and immunosuppressive activities, and can be used in gene cherapy. The human transporter proteins from the present invention are designated 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL and assays (e.g. chromosome mapping tissue typing, or in forensic biology), can dum enchodes encoding (I) can be used in screening predictive medicine (e.g. diagnostic assays, prognostic assays, cand in methods of treatment (e.g. therapeutic or prophylactic). (I) are production of 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084BL substrates or production of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084BL inhibitors. Disorders associated with 8099 and 46455, include disorders associated with sugar homeostasis (c.g. parkinson a disease or Alzahamer's disease or Algease), autonomic function or memory disorders (e.g. isolateria or age-related disorders) or learning cardiovascular disorders (e.g. isolatenia), or learning cardiovascular disorders (e.g. isolatenia reperfusion injury or crestenosis), hormonal disorders (e.g. hypothyroidism), were confirmed alsorders (e.g. chronic muccoutaneous candidiasis) dakctagaadagactacadagacatacaccagactacaccagacatradacracaradr 185 CGCCATCCTCAGCTTGGGCAACGTGCTCAACTACCTGGACAGGTACACCGTGGCAGGCGT 401 186 GGGGGGGCTGCTACATCACTCCTGAACTACATGGACGGCTTCACCGTGGCGCGT 245 402 CCTICTGGACATCCAGCAGCACTTTGGGGTCAAGGACCGAGGCGCCGGCCTGCTGCAGTC 461 9 Query Match
27.2%; Score 563.8; DB 6; Length 1587;
Best Local Similarity 64.3%; Pred. No. 8.7e-94;
Matches 879; Conservative 0; Mismatches 482; Indels 6; Sequence 1587 BP; 218 A; 529 C; 479 G; 361 T; 0 U; 0 Other; 342 282 126

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425 AGTGTTCATCTGTAGCTTCATGGTGGCTGCCCCCATCTTCGGCTACCTGGGCGACCGCTT 521 641 485 545 999 TGTCTTCCTTCGCCACGGGGGCCCTGGGCATGTGGATCCCGCTCTACCTGCACCGCGCCCA 1058 1115 1116 CCTCATCTTTGGGGCCATCACCTGCTTTACGGGATTTCTGGGCGTGGTCACGGGGGCGTGG 1175 1235 701 1085 761 605 821 665 GTCCCCTGTCCTGGCCATGATCACAGGAACACTCCTCATTCTGGTCCCAGCCACTAA 881 725 726 AAGGGGAGCCGTGGAGCGCCACTCAGATTTGCCACCCTGAACCCCACCTCGTGGTGGGC 785 966 845 1296 AGGAGCTATATCTGTATCTTCGTCGGGGAGGCCTGCTGTTTTCTAACTGGGCCATCAC 1355 965 AGACCTGATCCGCCAGAGCACTAAGGACTCCCCGCTCTGGGAGTTCCTGAGCCTGGGCTA 1535 CAACAGGAAGGTGATTCTCAGCTGCGGCATTTTCTTCTGGTCGGCCGTCACCTTCTCCAG CAArcedaaGrarcrcarerecedededearrecerricrestrecreereare CTCCTTCATTCCCCAGCAGTACTTCTGGCTGCTGGTCCTGTCCCGGGGGGTGGTGGGCAT CGGGGAGGCCAGCTACTCCACCATCGCCCCCACTATCATTGGCGACCTCTTCACCAAGAA dacaccederciades de des de contracte de contr CACGCGTACGCTCATGCTGCTTCTACTTCGCCATCCCACTGGGCAGTGGCCTGGG CTACATTACTGGCTCCAGCGTGAAGCAGGCAGCCGGAGACTGGCACTGGGCATTGCGGGT AAGGGGTCATGCCGACCAGCTCGGGGA---CCAGCTCAAGGCCCGGACCTCATGGCTCCG AGATATGAAGGCCCTGATTCGAAACCGCAGCTACGTCTTCTCTCCTCCTGGCCACGTCGGC AGTTGTGCA---GAAGACAGAGACGTGCAACAGCCCGCCCTGTGGGGCCAAGGACAG 906 cdradretradadaktecekeerreerreetadaaneretridererridereradada rcicaiciriscacroarcaccieceraceceaacroaceroaceroaceceracea 1176 AGCCACGCGCTGGTGCCGCCTGAAGACCCCAGGGGCCGACCCACTGGTGTGTGCCGTGGG 1026 GATCAGCCGCCGCCCCCCAACCCCCGGGCTGATCCCCTGGTCTGTGCCACTGG CATGCTGGGGTTCTGCTTCATCTGGCTGATCTTCGTGGCTGCCAAGAGCAGCATCGT 1146 Géccactriáriáritrcaitciricairidadadaccirccigiccardadiridedeciaiter 1206 gecceacatrorecretaledrearcatecrateceacecreteceacecricea GAGCTICACCICCCACCIGCTGGGGGACGCCGGGAGCCCCTACCICATTGGCTTTATCTC 486 246 462 306 522 366 582 426 642 702 762 909 822 999 939 882 996 1236 1416 1266 1476 ઠે 셤 ò 셤 ò 셤 à 셤 ò g 8 g ò 셤 à g ò a ò g ò g ò ద ò 원 à 셤 ò 셤 ò g 8 셤

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CGTGGTCCTTGGGGAGACCCCACCCTGCCTTCCCGGAGACTCCTGCTCTTCCTCTGACAG 965
 cDNA. Also included are a vector comprising the novel nucleic acid
                                                                                                                       Query Match
Best Local Similarity 64.3%;
Matches 879; Conservative (
                                                                                     transporter protein.
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TGACCGCCTGCGCCGGGAACTGGCCCCCCCTCTTGTCCGAGTTCCGGGCTCTGCAGTT 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising a cDNA encoding a human transporter protein, or its complement, a sequence that is 60 % identical to the cDNA, a fragment comprising at least 30 nucleotides of the cDNA, or a sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                                                                                                                                                Human, 88; gene; transporter; cytostatic; anorectic; antidiabetic; anticonvulsant; gene therapy; PGC-1 associated disorder; liver tumour;
                             CGCGCTCATGCTCTGCCCTTTCGTCGTGCTCCTGGGCGGCATGTTCTTCCTCGCCACTGC
                                                                   CATCTTCATTGAGGCCGACCGCCGGCGCACACTGCACGTGCAGG 1492
                                                       GCTCTTCTTCGTCAGCGACCGCCCAGGGCTGAGCAGCACCTGGGGG 1642
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                                                                                                                       BP,
                                                                                                                       ADD37479 standard; cDNA; 1587
                                                                                                                                                                               transporter 46455 cDNA
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2001US-00002769.
2001US-00024623.
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2000US-0256240P
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                                                                                                                                                                                                                                                                                                                                        19-SEP-2000;
25-SEP-2000;
14-NOV-2000;
15-DEC-2000;
11-DEC-2000;
21-DEC-2000;
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31-JUL-2001;
19-SEP-2001;
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14-MAY-2001;
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14-NOV-2001;
17-DEC-2001;
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molecule, producing the polypeptide, the isolated transporter and polypeptide, an isolated antibody that specifically binds to the polypeptide, an isolated antibody that specifically binds to the polypeptide, detecting the presence of the polypeptide or nucleic acid in a sample, a kit, identifying a compound that binds to, or that modulates the activity of, the polypeptide, and modulating the activity of the polypeptide acid is useful for preparing a composition for treating PGC-1 (not defined) associated disorders e.g. liver tumours, obesity, epilepsy or diabetes. The present sequence encodes a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 563.8; DB 10; Length
Pred. No. 8.7e-94;
0; Mismatches 482; Indels
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Silos-Santiago I;

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TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
, 2001US-00828035.
; 2001US-00833081.
; 2001US-00857683.
; 2001US-00957683.
; 2001US-00964252.
; 2001US-00964256.
                                                                                                         Glucksmann MA,
                                                                                    (MILL-) MILLENNIUM PHARM INC
                                                                                                                              2004-069000/07
                                                                                                                                         P-PSDB; ADI27957
                                          25-SEP-2001; 25-SEP-2001; 217-DEC-2001; 2
06-APR-2001;
11-APR-2001;
25-APR-2001;
19-SEP-2001;
                                                                                                          Curtie RAJ,
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Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                  AGGAGCCTATATCTGTATCTTCGTCGGGGAGACGCTGCTGTTTTCTAACTGGGCCATCAC
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                                            AGCCACGCGCTGGTGCCGCCTGAAGACCCAGGGGCCGACCCACTGGTGTGCCGTGGGG
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2000US-0185938P.
2000US-019593P.
2000US-0195993P.
2000US-019599P.
2000US-0233517P.
2000US-0235317P.
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2000US-0256588P.
2000US-0258028P.
2001US-00796720.
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03-MAR-2000;
07-APR-2000;
11-APR-2000;
26-APR-2000;
19-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,

CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

CC family (ICF) nucleic acids and proteins The TWIK-6, TWIK-7, IC23927,

TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC 53763 ICF nucleic acids and proteins may be used for preventing,

diagnosing and treating ICF-related diseases. The sequences may be used

CC contents and special and patient's genome that affect the activity of

mutations or deletions in a patient's genome that affect the activity of

CC patients own production of ICF proteins or to supplement the

CC patients own production of ICF proteins and in

CC anti-ICF protein of ICF protein expression and activity. The

antigens in the production of antibodies against ICF proteins and in

CC anti-ICF protein and activity. The antibodies may be used to

CC samples (e.g. by immunossasi). The nucleic acids and proteins may be used

CC samples (e.g. by immunossasi). The nucleic acids and proteins may be used

CC samples (e.g. by immunossasi). The nucleic acids and proteins may be used

CC samples (e.g. by immunossasi). The nucleic acids and proteins may be used

CC samples libepsy, hepatic disorders and cardivascular disorders.

CC samples libepsy, hepatic disorders and cardivascular disorders. This

CC sequence represents cDNA encoding the human 46455 protein of the

convention. Note: The sequence data for this patent is also available in

CC electronic format from USPTO at sequence.
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Example 1; SEQ ID NO 51; 638pp; English
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ADL61203 standard; DNA; 2165

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                      CGGGGAGGCCAGCTACTCCACCATCGCCCCCCATATCATTGGCGACCTCTTCACCAAGAA
                                  CTACATTACTGGCTCCAGCGTGAAGCAGCAGCCGGAGACTGGCACTGGGCATTGCGGGT
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polymucleotides and/or polymetides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. The molecules of the invention demonstrate cytostatic, antiangiogenic, vasotropic and vulnerary activities and may be useful in the field of pharmacogenomics, in particular for determining drug sensitivity and in treating breast cancer, hypervascular diseases, angiogenesis and scars in wound healing. The current sequence is that of a human protein tyrosine kinase biomarker DNA of the invention.
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                                           GTCCCCTGTCCTGGGCATGATCACAGGAACACTCCTCATTCTGGTCCCAGCCACTAA
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic.
immunosuppressant and cyrostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous allocalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anner diagnosis and therapy, drug screening, assaays for receptor activity, arner diagnosis and inflammation, leukaemias and sassays for receptor activity, arthritis and inflammation, leukaemias and Son Station of Son Station
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                                                                                                                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Paxinson's disease; huntington's disease; haemosteatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Pred. No. 9e-94;
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00488725.
25-ARR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-0059812.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00693036.
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27.2%;
Best Local Similarity 64.3%;
Matches 879; Conservative (
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SEQ ID
Human polynucleotide
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P-PSDB; AAM38697
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Human; transporter protein; anorectic; antidiabetic; anti-Parkinsonian; nootropic; neuroprotective; hypotensive; antidepressant; neuroleptic; cardiovascular; immunosupressive; gene therapy; sugar homeostasis; obesity; disabetes; anorexia; central nervous system disorder; depression; CNS disorder; Parkinson's disease; Alzheimer's disease; hypertension; autonomic function disorder; schizophrenia; learning disorder; amnesia; memory disorder; age-related disorder; cardiovascular disorder; ischaemia reperfusion injury; restenosis; hormonal disorder; hypothyroidism; hyperthyroidism; immune disorder; disorder; chronic mucocutaneous candidiasis; gene; ss.
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                                                                                                                GATCGTGCTGTCCCACCTGCTGGGTGATGCTGGGAGCCCCTACCTCATTGGCCTGATCTC
  AGACCTGATCCGCCAGAGCACTAAGGACTCCCCGCTCTGGGAGTTCCTGAGCCTGGGCTA
                                                                                 GAGCTTCACCTCCCACCTGCTGGGGACGCCGGGAGCCCCTACCTCATTGGCTTTATCTC
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/product= "46455 transporter
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18-DEC-2000; 2000US-0255588P.
21-DEC-2000; 2000US-0259028P.
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           or triangulture realization and interior present invention have anorette, antidiabletic, anti-Parkinsonian, present invention have anorette, antidiabletic, anti-Parkinsonian, cardiovascular and immonsuppressive activities, and can be used in gene therapy. The human transpotrer proteins from the present invention are designated 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL and 67084AL subscription of 8099, 46455, 54414, 53763, 67102, 44181, 67084FL or 67084AL subscription of treating disorders characterised by insufficient or excessive production of 8099, 46455, 54414, 53763, 67102, 44181, 67084FL or 67084AL subscription of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084AL subscription of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084AL subscription of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084AL subscription of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084AL subscription of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084AL are e.g. CNS disorders such as obesity, diabetes or anorexia. Disorders associated with sugar homeostasis cuch as obesity, diabetes or Alzheimer's disease, autonomic function disorders (e.g. hypertension, depression or schizophrenia), or learning or memory disorders (e.g. hypertension or schizophrenia), or learning cretenosis), hormonal disorders (e.g. hyporchyroidism or hyperthyroidism), cretenosis), hormonal disorders (e.g. hyporchyroidism or hyperthyroidism), cretenosis), crimune disorders (e.g. chronic muccoutaneous candidiasis)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising a cDNA encoding a human transporter protein, or its complement, a sequence that is encoding a human transporter protein, or its complement, a sequence that is 60 % identical to the CDNA, a fragment comprising at least 30 nucleotides of the CDNA, or a sequence encoding a fragment of the CDNA show included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated antibody that specifically binds to the polypeptide, an isolated antibody that specifically binds to the colypeptide, an isolated antibody that specifically binds to the colypeptide, an isolated antibody that binds to, or that modulates a sample, a kit, identifying a compound that binds to, or that modulates the activity of the polypeptide, and modulating the activity of the polypeptide, and modulating the activity of the colypeptide, and modulating a composition for treating PGC-1 (not defined) associated disorders e.g. liver tumours, coesity, epilopsy or diabetes. The present sequence encodes a novel human components protein.
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Pred. No. 9e-94;
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Best Local Similarity 64.3
Matches 879, Conservative
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                                                                                              19-SEP-2000;
25-SEP-2000;
05-OCT-2000;
14-NOV-2000;
15-NOV-2000;
15-DEC-2000;
18-DEC-2000;
22-JAN-2001;
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29-JUN-2001;
31-JUL-2001;
19-SEP-2001;
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17-DEC-2001
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                 anti-ICF protein antibodies, agoniets and antagoniets may be used to regulate ICF protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of ICF proteins in samples (e.g. by immunosasay). The nucleic acids and proteins may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Albraimer's disease, parkinson's disease, multiple sclerosis, epilepsy, hepatic disorders and cardiovascular disordere. This sequence represents obba encoding the human 46455 protein of the
identify modulators of ICF protein expression and activity. The
                                                                                                                                                                                                            invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCCGACATCGAGCAGTTCTTCAACATCGGGGACAGTAGCTCTGGGCTCATCCAGAC
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                                                                                                                                                                                                                                                                                    Sequence 2230 BP; 318 A; 752 C; 688 G; 472 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                         Human; 46455; gene; 88; ion channel family; ICF; cancer; leukaemia;
Alzhaimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease
                           1867
1821 CATCTTCATTGAGGCCGACGCGGGGGCACAGCTGCAGGTGCAGG
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2001US-00957683.
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P-PSDB; AD127957.
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26-APR-2000;
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25-SEP-2000;
25-SEP-2000;
15-DEC-2000;
11-DEC-2000;
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28-FEB-2001;
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25-APR-2001;
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are endical conditions e.g. by protein or gene therapy. The genes are calcated from a range of human tisues disclosed in the specification.

C isolated from a range of human tisues disclosed in the specification.

C the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic andemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

C ansemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

C multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

c cardiovascular disorders such as myocardial ischaemias; (d) wound healing

C infectious diseases e.g. cerebral anoxia and epilepsy; and (f)

infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

C from WIPO at ftp:wipo.int/pub/published_pct_sequences
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gastrointestinal, pulmonary, cardiovascular, renal and
                                                                                                                                                  Listing;
                                                                                                                                        NO 1236; 2081pp + Sequence
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1154 AAGGGGAGCCGTGGAGCGCCACTCAGATTTGCCACCCCTGAACCCCACCTCGTGGTGGGC 1095

Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive,

Birse CE, Rosen CA; WPI; 2002-122018/16. P-PSDB; ABB90265.

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1236 CATGCTGGGCTCTGCCATCTTCATCTGCCTGATCTTCGTGGCTGCCAAGAGCAGCATCGT 1295
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                                                                                                                                                                                                                                                                                                                           1059 AGTTGTGCA---GAAGACAGCAGAGACGTGCAACAGCCCGCCCTGTGGGGGCCAAGGACAG 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1176 AGCCACGCGCTGGTGCCGCCTGAAGACCCAGGGGCCGACCCACTGGTGTGTGCCGTGG 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1416 GAGCTTCACCTCCCACCTGCTGGGGACGCCGGGGCCCCTACCTCATTGGCTTTATCTC 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1476 AGACCTGATCCGCCAGAGCACTAAGGACTCCCCGCTCTGGGAGTTCCTGAGCCTGGGCTA 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           674 GGCCGACATTCTGCTGTACGTGTGATCCCTACCGACGCTCCACCGCCGAGGCCTTCCA 615
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                                                                                                                                                                                                                             1034 TGTGGCCTTTGTCACGGGCTCCCTGGCTCTGTGGGCTCCGGCATTCCTGCTGCGTTCCCG 975
939 AGATATGAAGGCCCTGATTCGAAACCGCAGCTACGTCTTCTCCTCCCTGGCCACGTCGC 998
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GURRENT FILING DATE: 1998-03-06
GRALIER APPLICATION NUMBER: 06/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER PLICATION NUMBER: 60/040,336
EARLIER PLICATION NUMBER: 60/040,531
EARLIER PLILING DATE: 1997-05-23
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                3 US-09-103-840A-1

3 US-09-103-840A-2

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3 US-09-060-756-4

4 US-09-670-314-4

4 US-09-298-568-3

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4 US-09-894-273-3

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4 US-09-774-528-438

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Sequence 16, Appl
Sequence 15609, A
Sequence 15645, A
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Sequence 93,
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US-09-128-155-16
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R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/048,974

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/056,886

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,887

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R APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,670 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 APPLICATION NUMBER: 60/056,862 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/048,964 LING DATE: 1997-05-23 LING DATE: 1997-08-22 LING DATE: 1997-08-22 LING DATE: 1997-05-23 LING DATE: 1997-08-22 EARLIER I EARLIER I EARLIER EARLIER EARLIER EARLIER SARLIER SARLIER SARLIER

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Patent No. 6420526

GENERAL INFORMATION:

APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-09-08

EARLIER RAPPLICATION NUMBER: EVT/US98/04493

EARLIER PILING DATE: 1998-03-06

EARLIER PILING DATE: 1998-03-06

EARLIER PILING DATE: 1998-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
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REFLICATION NUMBER: 60/043,699
REPLICATION NUMBER: 60/043,669
RETLING DATE: 1997-04-11
RETLING DATE: 1997-04-11
RETLING DATE: 1997-04-11
RETLING DATE: 1997-04-11
REPLICATION NUMBER: 60/043,313
RETLING DATE: 1997-04-11
RETLING DATE: 1997-04-11 R APPLICATION NUMBER: 60/056, 893
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 830
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056, 878
R PILING DATE: 1997-08-22
R PILING DATE: 1997-08-22
R PILING DATE: 1997-08-22
R PILING DATE: 1997-08-22
R PILING DATE: 1997-08-22 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,592

RR FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,581

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,584

R APPLICATION NUMBER: 60/047,584

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,587

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,492

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,598

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,592

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,612

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,601

R FILING DATE: 1997-05-23 R PLING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,568

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R PLING DATE: 1997-04-11

R PLING DATE: 1997-04-11

R PLING DATE: 1997-04-11

R PPLICATION NUMBER: 60/043,311

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R FILING DATE: 1997-04-11

R PPLICATION NUMBER: 60/043,671 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/047,503 EARLIER
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EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER APPLICATION NUMBER: 60/043,578
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EARLIER PILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER APPLICATION NUMBER: 60/043,576
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EARLIER PILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043,670
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,875
R APPLICATION NUMBER: 60/056,862
R APPLICATION NUMBER: 60/056,862
R APLING DATE: 1997-08-22
R APLICATION NUMBER: 60/056,887
R FILING DATE: 1997-08-22 R APPLICATION WUMBER: 60/056,888
R FILING DATE: 1997-08-22
R APPLICATION WUMBER: 60/056,879
RR FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,994
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,636
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,874
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/047,599
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,588
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,585
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,586 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,589
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,595 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/057,761 LING DATE: 1997-08-22 FILING DATE: 1997-08-22 LING DATE: 1997-08-22 EARLIER PEARLIER FEARLIER FEAR EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I

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               780 GAGATCAGCCGCCGGYTCCGCCACTCCAACCCCCGGGCTGATCCCCTGGTCTGTGCCCACT
                                                                                                                                                                    1294 GTAGGAGCCTATATCTGTATCTTCGTCGGGGAGACGCTGCTGTTTTCTAACTGGGCCATC
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GENERAL INFORMATION:

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT APPLICATION NUMBER: D20/149,476

CURRENT APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-09-08

EARLIER FILING DATE: 1998-09-08

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-05-23

EARLIER FILING DATE: 1997-05-23
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Pred. No. 9.5e-95;
3; Mismatches 425;
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05.
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05.
EARLIER PELICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-06-13
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BARLIER PELLORATION NUMBER: 60/045, 505
BARLIER PELLORATION NUMBER: 60/065, 605
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             781 GAGACCCTCCTGTCCATGAACTGGGCCATCGTGGCCGACATTCTGCTGTACGTGGTGATC 840
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,768
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CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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INPORMATION POR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-232-463-14/c
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21.9%; Score 453; DB 4; Length 14
Best Local Similarity 65.2%; Pred. No. 9.4e-83;
Matches 716; Conservative 0; Mismatches 375; Indels
                                                EARLIER FILING DATE: 1997-08-27
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-08-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-12
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/056,908
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LCCATION: (1)...(152231)

COTHER INFORMATION: n = A,T,C or G

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| Sequence 48, Application US/09616289
| Patent No. 6632923
| GENERAL INFORMATION:
| APPLICANT: Lee8, Ann M. |
| APPLICANT: Lee8, Ann M. |
| APPLICANT: Lee8, Robert S. |
| APPLICANT: Lee8, Ann M. |
| TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING |
| TITLE OF INVENTION: NOVEL LOW OFFICE SOFT |
| TITLE OF INVENTION: ATHERNOSCLEROSIS |
| TITLE OF INVENTION: ATHERNOSCLEROSIS |
| TITLE OF INVENTION: ATHERNOSCLEROSIS |
| FILE REFERENCE: 10797-004001 |
| CURRENT APPLICATION NUMBER: US 09/517,849 |
| PRIOR PILING DATE: 2000-03-02 |
| PRIOR FILING DATE: 1996-11-27 |
| NUMBER OF SEQ ID NOS: 53 |
| SOFTHARE PREESED FOR WINDOWS VERSION 4.0 |
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                                                                                                        13; Conservative 189; Mismatches
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Best Local Similarity 53.8
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; LOCATION: (246)...(1895)
US-09-616-289-48
                                                    Best Local Similarity
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US-09-616-289-48/c
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LENGTH: 2561
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"Sequence 15609, Application US/09252991A
| Sequence 15609, Application US/09252991A
| Sequence 15609, Application US/09252991A
| Sequence 15609, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al. |
| APPLICANT: Marc J. Rubenfield et al. |
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| FILE REFERENCE: 107196,136 |
| PRIOR PILING DATE: 1999-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-07-27
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; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: NOVER: US/09/128,155
; CURRENT APPLICATION NUMBER: US 60/091,650
; EARLIER PILING DATE: 1998-07-02
; EARLIER PILING DATE: 1998-07-02
; EARLIER PILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16--
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General 1709, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15009
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Sequence 15645, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

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Pred. No. 0.0024;
0; Mismatches 253; Indels 9
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Best Local Similarity 47.5
Matches 241; Conservative
NUMBER OF SEQ ID NOS:
SEQ ID NO 15609
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US-09-252-991A-15609
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ORGANISM: 1
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2.9%; Score 59.8; DB 3; Length 319;
Best Local Similarity 53.7%; Pred. No. 0.0021;
Matches 124; Conservative 0; Mismatches 107; Indels
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Sequence B, Application US/09165264

Patent No. 619510

GENERAL NO. 619510

TITLE OF INVENTION:

PILE REFERENCE: 4471001

CURRENT APPLICATION WALLI-Loci Genomic Analysis

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 14

SEQ ID NO BLEATH OF VERY 2.1

SEQ ID NO BLEATH OF VERY 2.1

LENGTH: 319
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; Sequence 7, Application US/09165264
; Patent No. 6197510
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2.9%; Score 59.8; DB 3;
Best Local Similarity 54.9%; Pred. No. 0.0021;
Matches 118; Conservative 0; Mismatches 97;
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APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analyais
FILE REFERENCE: 44747
CURRENT APPLICATION UNMBER: US/09/165,264
CURRENT APPLICATION UNMBER: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 320
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55.2%; Pred. No. 0.0026;
tive 0; Mismatches 9
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ORGANISM: Artificial Sequence
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THEIR USE IN DIAGNOSING AND TREATING
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR PLING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-26
PRIOR PLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SEQ ID NOS: 53
SEQ ID NOS: 53
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52.2%; Pred. No. 0.0045;
ive 0; Mismatches 122; Indels
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; OTHER INFORMATION: Incyte ID No. 6673549 221042.1
US-09-976-594-1091
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; Sequence 1091, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
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Best Local Similarity 52.2
Matches 133; Conservative
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US-09-616-289-50
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 2030
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Manchal A.
APPLICANT: Lees, Manchal A.
APPLICANT: Law, Sanca M.
APPLICANT: Arjona, Anabal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR PELING DATE: 2000-07-44
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-27
PRIOR PELING DATE: 1997-11-27
PRIOR PELING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
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2.9%; Score 59.8; DB 4; Length 1614;
Best Local Similarity 52.2%; Pred. No. 0.0029;
Matches 133; Conservative 0; Mismatches 122; Indels 0
      231 GACCGGACCCCCGGCACCCCCG 253
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
                                                                                                                                                        Sequence 45, Application US/09616289
Patent No. 6632923
                                               107 GGNNTCTCCCAGCGGCCGCCTCG
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; LOCATION: (1)...(1614)
US-09-616-289-45
                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
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Search completed: October 23, 2004, 12:53:52 Job time : 191 secs

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October 23, 2004, 08:18:17; Search time 1000 Seconds (without alignments) 10611.640 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/USO6_WWW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_WWW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_WWW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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2071
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Query e Match Length DB ID Description	100.0 2071 16 US-10-085-198-47	73.7 3179 15 US-10-168-651-36	27.2 1587 13 US-10-024-623-6		27.2 1587 15 US-10-146-733-51	27.2 2165 17 US-10-648-593-127	27.2 2218 13 US-10-098-841-56	27.2 2230 13 US-10-024-623-4	27.2 2230 15 US-10-154-419-54	27.2 2230 15 US-10-146-733-49	27.2 2264 9 US-09-833-381-883	
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Sequence 245, App Sequence 245, App Sequence 245, App	246,	Sequence 246, App Sequence 246, App	87, A	87,	87,	Sequence 51, Appl	3, AI	Sequence 50, Appl	Sequence 1, Appli	Sequence 5978, Ap	Sequence 136, App	39,	Sequence 146, App								Ξ	8	ö	H	ï	Sequence 519, App	급		Sequence 148749,
US-09-809-391-245 US-09-882-171-245 US-10-164-861-245	US-09-809-391-246	US-U9-882-1/1-246 US-10-164-861-246	US-09-809-391-87	US-09-882-171-87	US-10-164-861-87	US-10-403-571-51	US-09-860-232A-3	US-10-297-022-50	US-09-860-232A-1	US-09-918-995-5978	US-10-169-395-136	US-10-168-651-39	US-10-169-395-146	US-10-027-632-151511	US-10-027-632-151511	US-09-826-734-245	US-09-918-995-6080	US-10-108-260A-847	US-09-826-734-159	US-09-826-734-131	US-09-918-995-13260	US-10-097-065-29	US-10-372-876-29	US-10-097-065-124	US-10-372-876-124	US-10-283-975A-519	US-10-242-535A-11760	US-10-085-783A-11760	US-10-027-632-148749
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26.2	24.7	24.7	21.9	21.9	21.9	21.6	21.0	21.0	21:0	18.8	17.8	17.8	17.8	16.7	16.7	16.0	15.7	12.7	12.2	11.7	10.3	10.3	10.3	9.3	9.3	9.0	8.1	8.1	8.1
542.8 542.8	512.4	512.4	453	453	453	447.6	434.6	434.6	434.6	388.8	368	368	368	346.6	346.6	331.4	324.8	263.2	251.8	242.4	214	213.8	213.8	193	193	187.4	168.4	168.4	167.8
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## ALIGNMENTS

Sequence 47, Application US/10085198
Sequence 47, Application US/10085198
Publication No. US2004009907A1
GENERAL INFORMATION:
APPLICANT: Alsobrook et al.
TITLE OF INVENTION:
FILE REFERENCE: 21402-215
CURRENT APPLICATION NUMBER: US/10/085,198
CURRENT APPLICATION NUMBER: 60/271,646
PRIOR APPLICATION NUMBER: 60/271,646
PRIOR APPLICATION NUMBER: 60/271,646
PRIOR APPLICATION NUMBER: 60/271,646
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
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PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-27
PRIOR PILING DATE: 2001-03-27
PRIOR PILING DATE: 2001-03-27
PRIOR PILING DATE: 2001-03-20

	16; Length 2071;  Oy 1021 CTGGGCATGTGGATCCCGCTCTACCTGCACCGCGCCCAAGTTGTGCAGAAGACAGCAGAG 1080	09 90990        09 90990	CGCAG 120 QY 1141		GACCC	AGCAG	70 - 70 - 70 - 70 - 70 - 70 - 70 - 70 -	AGCAG			AGCAG	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	16CTG	CCAGC 78			
TYPE: DNA ORGANISM: Homo sapiens 10-085-198-47	., н	SCCGCCATGATGTGCCTGGA 	61 GGCGCGCGGAGGAGGAGGCGGAGCGGGAGCGGCGCGCGGCG		181 GCCGCGGGCGATGAGGTGCAGACGCTGTCGGGCAGCGACCGAC	241 CCGGGACCCCGGGACCCCGGCTGGCAGCTACTGCAAAGGGCCCCGGGCTC	301 CCCAAACGGGCCAGCTTGGGCCGCGGGGGGGGGGCGCCGCGCGCG	361 AACGTGCTCAACTACCTGGACAGGTACACCGTGGCAGGCGTCCTTCTGGACATCCT 	421 CACTTTGGGGTCAAGGACCGAGGCGCCGCCTGCTGCGGTTCTTGTAGTTTCTTGTAGTTTC	481 ATGGTGGCTGCCCCATCTTCGGCTACCTGGGCGACCGCTTCAACAGGAGGTGA 	541 AGCTGCGGCATTTTCTTCTGGTCGGCGGTCACCTTCTCCAGGTCCTTCATTCCCC 	601 TACTTCTGGCTGCTGGTCCTGTCGGGGGTGGTGGGGCATCGGGGAGGCCACCT 	661 ACCATCGCCCCACTATCATTGGCGACCTCTTCACCAAGAACACGCCTACGCTCATCATCATCATCATCATCATCATCATCATCATCATCA	721 TCCGTCTTCTACTTCGCCATCCCACTGGGCAGTGGCCTGGGTACATTACTGGCT 	781 GTGAAGCAGGCAGCCGAGACTGGCACTGGGCATTGCGGGTGTCCCTGTCCTGGGCATG	841 ATCACAGGAACACTCATCCTCATTCTGGTCCCAGCCACTAAAAGGGGTCATGCCGA 	901 CTCGGGGACCAGCTCAAGGCCCGGACTCATGGCTCCGAGATATGAAGGCCCTGATTCGA

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Db 361 CCGCCTIGCTGCAGTCAGTTTCATCTGTAGCTTCATGGTGGCTGCCCCCATCTTCGGCT 42	Qy 506 ACCTGGGCTCAACAGGAAGGTGATTCTCAGCTGCGGCATTTTCTTCTGGTCG 565	Db 421 ACCTGGGCGACCGCTTCAACAGGAAGGTGATTCTCAGCTGGGGCGATTTTCTTCTTCTGGTCGG 480	Qy 566 CCGTCACCTTCTCCAGCTCCTTCATTCCCCAGCAGTACTTCTGGCTGCTGGTCCTGTCCC 625	Db 481 CGTCACCTTCTCCAGCTCCTTCATTCCCCAGCAGTACTTCTGGCTGCTGGTCCTGTCCC 540	Qy         626         GGGGGCTGGTGGCATCGGGGAGGCCAGCTACTCCACCACCACTATCATTGGCG         685           nh         641         [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	531 GGGGGCIGGGGCAICGGGGGGCCCAGCIACICCACCAICGCCCCCCCC	601 ACCTCTTCACCAAGAACACGCGTACGATGCTGCTGTCTTCTACTTCGAC 66	Qy 746 TGGGCAGTGGCCTGGGCTACATTACTGGCTCCAGCGTGAAGCAGGCAG	1000-NOT TOOCHOLOGOCTION TIME TOOLING ON THE TOOLING ON TOOLING ON THE TOOLING ON	721 ACTGGGGTGTCCCCTGTCCTGGGCATGATCACAGGAACACTCATCCTCATTC 78	92	58; Db 781 TGGTCCCAGCCACTAAAAGGGGTCATGCCGACCAGCTGGGGGACCAGGTCCAGGCCCGGA 840	Qy 926 CCTCATGGCTCCGAGATATGAAGGCCCTGATTCGAAACCGCAGCTACGTCTTCTCCTCCC 985	Db 841 CCTCATGGCTCCGAGATATGAAGGCCCTGATTCGAAACCGCAGCTACGTCTTCTCCTCCC 900	Oy . 986 TGGCCACGTCGGCTGTCTCGCCACGGGGCCCTGGCATGTCGATCCGGTCTACC 104	Db 901 TGGCCACGTCGGCTGTCTCGCCACGGGGCCCTGGGGCATGTGGATCCCGCTCTACC 960	Qy         1046         TGCACCGCGCCCAAGTTGTGCAGAAGACAGACGTGCAACAGCCGCCCGC	Qy         1106         CCAAGGACAGCCTCATCTTTGGGGCATCTTATGGGGATTTCTGGGCGTGGTCA         1165	1166 CGGGGCAGGAGCCACGCGCTGGTGCCGCCTGAAGACCCAGCGGGCCGACCCACTGGTGT	1081 CGGGGCAGGAGCCACGCGCTGGTGCCGCCTGAAGACCCAGCGGGCCGACCCACTGGTGT	QY         1226 GTGCCGTGGGCATGCTGCCATCTTCATCTGCCTGATCTTCGTGGCTGCCAGA 1285	Oy 1286 GCAGCATCGTAGGAGCCTATATCTGTAGGGAGACGCGGGAGACGCTGCTGTTTCTAACT 134	Db 1201 GCAGCATCGTAGGAGCCTATATCTGTTCGTCGGGGAGACGCTGCTGTTTTCTAACT 126	03	1406 TRACCHACATACATACATACATACATACATACAGAGAGACACACAC	1321 TGGCCTTGCAGAGCTTCACCTCCCACCTGCTGGGGGACGCCCGGGAGCCCCTACCTCATTG	Oy 1466 GCTTTATCTCAGACCTGAGGCACTAAGGACTCCCGGTCTGGGAGTTCCTGA 152 	このはことは、	T
Db 2041 GCTCACGGTGGCTATCACGGTCCCTGCTTCC 2071	RRSITL'F 2		; Publication No. US20030171275A1	; APPLICANT: INCYTE GENOMICS, INC. ; APPLICANT: BAUGHN, Mariah R.	; APPLICANT: BURFORD, Neil ; APPLICANT: AD-YOUNG, Janice ; APPLICANT: LU. Doung Aira M.		HILLMAN		; APPLICANT: GANDHI, Ameeni R.; APPLICANT: TANG, Y. Tom	; APPLICANT: KHAN, Farrah A. ; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS	; FILE REFERENCE: PI-0005 PCT ; CURRENT APPLICATION NUMBER: US/10/168,651 ; CIRENT PITING DAFF: 2002.66-21	176,083; 60/177,332; 60/178,572; 60/179,7	; PRIOR FILLIG DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02; ; 2000-02-10	NUMBER OF SEQ ID NOS: 54	(1) (1)	; TYPE: DNA ; ORGANISM: Homo sapiens	; FEATURE: ; NAME/KEY: misc_feature ; OTHER INFORMATION: Incyte ID No. US20030171275A1 3232992CB1	Ouery Match 73.7%; Score 1525.8; DB 15; Length 3179; Best Local Similarity 99.7%; Pred. No. 0;	Matches 1549; Conservative 0; Mismatches 2; Indels 2; Gaps	QY         88         GCGGAGCGCGCCGGCGCCCGGGGGCGCAGCGAGCGGCTGCCGGTTGCTGC         147           D         1	GGGCCCGGGGCGCGGCGCGCGGGAGTCTCGGCCGCGGGCGATGAGGTGCAGACGCTG 20	bl GedelleCodeseColoeseCostateseCottaseCottaseCottaseCottaseContractaseCottaseC	121 TCGGGCAGCGTAAGGCGGGCCCCGACCGGGCACCCCCGGCACCCCCGGCTGC	32	Db 181 GCAGCTACTGCAAAGGGCCCCCGGCGCTCAGCAGCCCAAACCGGCCAGCTTGGGCCGCGG 240	Oy 327 GCGGGGGC-AGCCGCCGATCCTCAGCTTGGGCAACGTGCTCAACTACCTGGACAGGT 385  DA 241 GCGGCGGCAACGCCATCCTCAGCTTGGGCAACGTGCTCAACTACCTGGACAGGT 385	386 ACACCGTGGCGGCGTCCTTCTGGACATCCAGCACTTTGGGGTCAAGGACCGGGGGG	Db 301 ACACCGTGGCAGGCGTCCTTCTGGACATCCAGCACTTTGGGGTCAAGGACCGAGGCG 360	

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Sequence 56, Application US/10154419
Sequence 56, Application US/10154419
Publication No. US20030143675A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gluckeman, Maria Alexandra
APPLICANT: Myers, Rachel E.
TITLE OF INVENTION: NOVEL 87259, 67112, 53659, 57250, 63760, 49938, 32146,
TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,
TITLE OF INVENTION: AND 57255A1 MOLECULES AND USES THEREFOR FILE REPERENCE: MAI-249
CURRENT APPLICATION NUMBER: US/10/154,419
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Sequence 6, Application US/10024623

Publication No. US202020187524A1

GENERAL INFORMATION:

APPLICANT: CUTties, Rory A.J.

ITILE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF TITLE OF INVENTION: 1058 THEREOF

TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

TITLE OF INVENTION: USE THEREOF

CURRENT APPLICATION NUMBER: US 60/256,240

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LENGTH: 1587
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| Sequence 51, Application US/10146733
| Publication No. US2000105893A1
| Publication No. US2000105893A1
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| Publication No. US200010589A1
| Publication No. US200010589A1
| Publication No. US200010589A1
| Publication No. US20001059A1
| Publication No. US20001059A1
| TITLE OF INVERTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
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| PRIOR PLICATION NUMBER: US 60/185, 938
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| PRIOR PLICATION NUMBER: US 60/195, 734
| PRIOR PLICATION NUMBER: US 60/195, 734
| PRIOR PLICATION NUMBER: US 60/195, 739
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                                            966 ICTCATCTTTGGACTCATCACCTGCCTGACCGGAGTCCTGGGTGTGGA
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CURRENT FILING DATE: 2002-05-22
Prior Application removed - See Number OF SEQ ID NOS: 99
SOFTWARE: FastSEQ Version 4.0
SEQ ID NO 56
LENGTH: 1587
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.39
Matches 879; Conservative
                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                            ... (1587)
                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1).
US-10-154-419-56
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Sequence 127, Application US/10648593
Publication No. US20040106132A1
GENERAL INPORMATION:
TELL INPORMATION:
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
TITLE OF INVENTION: UNMBER: US/10/648,593
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR PRILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
NUMBER OF SEQ ID NOS: 557
SEQ ID NO 127
SEQ ID NO 127
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27.2%; Score 563.8; DB 15;
Best Local Similarity 64.3%; Pred. No. 5.6e-133;
Matches 979; Conservative 0; Mismatches 482;
                 PRIOR APPLICATION NUMBER: US 60/258,028
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 09/796,720
PRIOR APPLICATION NUMBER: US 09/80,035
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 09/83,128
PRIOR APPLICATION NUMBER: US 09/957,683
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
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ORGANISM: Homo sapiens
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US-10-146-733-51
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APPLICANT: Wang, iungling
APPLICANT: Wang, Oing A.
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Rui-hong
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Diwei
APPLICANT: Dian, Xiaohong B.
APPLICANT: Diang, Xiaohong B.
APPLICANT: Wang, Xiaohong B.
APPLICANT: Diang, Xiaohong B.
APPLICANT: Wang, Xiaohong B.
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APPLICANT: Diang, Xiaohong B.
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APPLICA
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Publication No. US2002019767941
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, Vinod
APPLICANT: Xu. Chongiun
APPLICANT: Xu. Chongiun
APPLICANT: Xn. Yunging
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Zhoo, Oing A.
APPLICANT: Chen, Rui-hong
APPLICANT: Rang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
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; LOCATION: (372)..(1958)
US-10-098-841-56
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RESULT 9

US-10-154-419-54

Sequence 54, Application US/10154419

Sequence 54, Application VUS20030143675A1

Sequence 54, Application No. US20030143675A1

GENERAL INFORMATION:
APPLICANT: CULTIS, NOTY A.J.
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachal E.
TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,
TITLE OF INVENTION: 67076, 67102, 44181, 67084ALT, FBH58295FL, 57255,
TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR
TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR

TITLE OF INVENTION NUMBER: US/10/154,419

CURRENT APPLICATION NUMBER: US/10/154,419

CURRENT RILING DATE: 2002-05-22

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSEQ Version 4.0

EDUCATION: APPLICATION OF APPLICA
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Pred. No. 5.8e-133;
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27.2%;
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US-10-154-419-54
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Pred. No. 5.8e-133;
0; Mismatches 482;
PRIOR APPLICATION NUMBER: US 60/195,993
PRIOR FILING DATE: 2000-04-11
PRIOR PLLING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/199,799
PRIOR APPLICATION NUMBER: US 60/235,018
PRIOR PILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-25
PRIOR PLLING DATE: 2000-09-25
PRIOR PLLING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US 60/256,240
PRIOR PLLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/256,028
PRIOR APPLICATION NUMBER: US 60/256,038
PRIOR PLLING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 69/83,081
PRIOR PLLING DATE: 2001-04-11
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PRIOR PLLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 69/964,256
PRIOR APPLICATION NUMBER: US 69/964,256
PRIOR PLLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 69/964,256
PRIOR PLLING DATE: 2001-09-25
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Best Local Similarity 64.3%;
Matches 879; Conservative 0
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; LOCATION: (376)...(1962)
US-10-146-733-49
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ORGANISM: Homo sapiens
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Sequence 49, Application US/10146733

Publication No. US20030165891A1

GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria A.
APPLICANT: Glucksmann, Maria A.
TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
TITLE OF INVENTION: HWMD-1, TWIK-6, alpha2delta-4, 54414, AND 53763 MOLECULES
TITLE OF INVENTION: MUMBER: US/10/146,733
CURRENT APPLICATION NUMBER: US 60/185,938
FRIOR PELING DATE: 2000-02-29
PRIOR PILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-03-03
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FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT APPLICATION NUMBER: US/09/833,381
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOUTHWARE: FESTES
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; OTHER INFORMATION: n = A,T,C
US-09-833-381-883
                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Sequence 883, Application US/09833381 Patent No. US20020132090A1 GENERAL INFORMATION: APPLICANT: Robison, Keith E.

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US-10-264-237-1236/C
; Sequence 1236, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
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; TILE OF INVENTION:
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; TILE OF INVENTION:
; CURRENT PILING DATE: 2002-10-04
; PRIOR PAPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR PILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIN Ver. 3.1
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
FRIOR APPLICATION NUMBER: 09/809,391
FRIOR APPLICATION NUMBER: 09/149,476
FRIOR APPLICATION NUMBER: 09/149,476
FRIOR APPLICATION NUMBER: PCT/US98/04493
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Publication No. US20030175858A1
GENERAL INFORMATION:
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Fublication No. US20030049618A1
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 2201
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Pred. No. 1.2e-127;
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Best Local Similarity 64.3%;
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1998-03-06 NUMBER: 60/040,162 1997-03-07 1997-03-07 NUMBER: 60/038,621 1997-03-07 NUMBER: 60/040,626 1997-03-07 NUMBER: 60/040,334 1997-03-07 NUMBER: 60/040,336 1997-03-07 1997-03-07 NUMBER: 60/040,463 1997-03-07 NUMBER: 60/040,163	(1) (6) (047, 1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	5-23 60/047,586 60/047,586 5-23 60/047,596 60/047,596 60/047,596 60/047,596 60/047,596 60/047,606 60/047	NUMBER: 60/043,568 1997-04-11 1997-04-11 NUMBER: 60/043,314 1997-04-11 1997-04-11 1997-04-11 NUMBER: 60/043,311 NUMBER: 60/043,674 1997-04-11 1997-04-11 1997-04-11
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Publication No. US/0030225248A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
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RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,589
RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,593
RR FILING DATE: 1997-05-23
RR PILING DATE: 1997-05-23
RR PLING DATE: 1997-05-38
RR PLING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                         DR APPLICATION NUMBER: 60/056,664

DR FILING DATE: 1997-08-22

DR FILING DATE: 1997-08-22

DR APPLICATION NUMBER: 60/056,881

DR APPLICATION NUMBER: 60/056,881

DR APPLICATION NUMBER: 60/056,881

DR APPLICATION NUMBER: 60/056,909

R FILING DATE: 1997-08-22
                                                                                                                                                                               APPLICATION NUMBER: 60/043,576
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
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APPLICATION NUMBER: 60/056,884
FILING DATE: 1997-08-22
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FILING DATE: 1997-09-05
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                                                                                                                                                                              Score 542.8; DB 15;
Pred. No. 1.2e-127;
1; Mismatches 478;
                                                                                                                                                                               DB 15;
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR PELLING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR PLING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SEQ ID NO 245
                                                                                                                                                                               Query Match
Best Local Similarity 64.3%;
Matches 877; Conservative
                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                    LENGTH: 2201
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earch completed: October 23, 2004, 13:10:35 ob time : 1006 secs

OM nucleic

Run on:

Sequence:

Searched:

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Location/Qualifiers

1. .68
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/clone="UI-E-E00-ahy-f-02-0-UI"
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/dab_host="DH108 (Life Technologies) (T1 phage resistant)"
/clone lib="UI-E-E00"
/clone lib="UI-E-E00"
/note="Grgan: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-E00 is a cDNA library containing the following tissue(s): fetal eye. The library was constructed
            CR614611 Full-Teng
AK008721 Mus muscu
BQ893216 AGENCCURT
BE380495 601270572
AK020683 Mus muscu
BU377598 6013810820
BX523238 BXE32338
BM570349 1108907. y
BB840028 BB840028
BE914111 601.665234
BE91411 601.665234
BE912612 60166363
CR611391 full-leng
BG244390 602356517
AK041376 Mus muscu
BM794641 K-EST0076
BU44260 LEZINIS97
AK033907 Mus muscu
CD676225 f833906.y
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Fax: 319 315 9565

Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Seq primer: M13 Reverse.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-E-EOO-ahy-f-02-0-UI.rl UI-E-EOO Homo sapiens cDNA clone
UI-E-EOO-ahy-f-02-0-UI 5', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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AXC20683
BAC20683
BAC20683
BE523238
BB523238
BB514111
BB512612
CR611391
CR611391
AC41376
AC41337
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BI410266 602966259
BI414356 60290376
CN528616 UI-M-HQ0-
CK479120 AGENCOURT
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                                          32.2%; Score 666; DB 4; Length 668; 99.7%; Pred. No. 5.7e-125; ive 0; Mismatches 2; Indels
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DEFINITION ACCESSION VERSION

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                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 958)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NGT-CGAP clone distribution information can l

found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAMI1296 row: f column: 15

High quality sequence etart: 13

High quality sequence stop: 850.

Location/Qualifiers
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85.2%; Pred. No. 4.7e-121;
tive 0; Mismatches 127; Indels 2
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/strain="CZECH II"
Mus musculus (house mouse)
Mus musculus
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/lab_host="DHIOB (phage-resistant)" /clone lib="NCI CGAP Lul3" /clone lib="NCI CGAP Lul3" /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site 1: NotI; Site 2: EcoRI; lst strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCCTCTGTTTTTTTTTT	Query Match         30.5%;         Score 630.8;         DB 4;         Length 924;           Best Local Similarity         86.5%;         Pred. No. 8.4e-118;         Indels         6;         Gaps           Matches 754;         Conservative         0;         Mismatches 112;         Indels         6;         Gaps           Qy         755         GCCTGGGCTACATTACTGGCTCCAGCGTGAAGCAGCCGGAGACTGGCACTGGGC         8         GGCTGGGTATATCACAGGTTCCAGCGTTGAAGCAGGCAGCTGGAACTGGGCATTGGGC         6	813 68 873 128 933	93 GCCCAAGTTGTCCCTCGCCAGGGGCCTGGGCATGTGGATTCCCCTCTATCTTCGCGGGGGGGG	548 1353 607 1413 667 1473 726 1533
	1426 TCCCACCTGGGGGAGCCCGGGAGCCCTTATTGGCTTTATCTCAGACCTGATC  1606 TCCCATCTGGGGGAGCCCGGGAGCCCCTACTGGCTTTATCTCAGACCTGATC  1606 TCCCATCTGGGGGGAGCGCTGGGAGCCCCTATTGGCTTTATCTCGGACCTAATC  1486 CGCCAGAGCACTAAGGACTCCCCGGTTCTGGGGTTCTGGGGTTAGTTTGGTTATCTTGGGCTTAATCTAATC  1606 TCCCAGAGCACTAAGGACTCCCCGTTTGGGGTTCCTGGGGTTAGTGGTTATGTTTATCTTGGGTTATGTTATTTTTTTT	1546 CTCTGCCCTTTCGTCGTGGCGGCA-TGTTCTTCCTCGCCACTGGGCTCTTCTT  726 CTGTGCCCTTTTGTCGTGGTCCTGGGCGGCA-TGTTCTTCCTCGCCACTGGGTCTTCTT  1605 CTCTGGCGCTGTGGTCCTGGGTGGATTGTTTCTTCTTGCATTGTTTTTTTT	HEBSULT 3 B1414356 LOCUS LOCUS B1414356 LOCUS DEFINITION G02990376F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146410 5', MRNA sequence. ACCESSION B1414356 B1414356.1 GI:15175279 B1414356 B141435 B1414356 B1414356 B1414356 B1414356 B1414356 B1414356 B1414356	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by:Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI1361 row: g column: 19 High quality sequence start: 10 High quality sequence stop: 824. Location/Qualifiers Location/Qualifiers 1. 924 /organism="Mus musculus" /mol_type="mRNA" /gtrain="CZEGH" /db_xref="mRNA" /db_xref="mRNA" /dlone="IMAGE:5146410" /tissue_type="pooled lung tumors"

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                                                                                                                                                       30.5%; Score 630.8; DB 4; Length 924; ity 86.5%; Pred. No. 8.4e-118; Bervative 0; Mismatches 112; Indels 6.
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AGENCOURT 17583048 NIH MGC_232 Rattus norvegicus cDNA clone
IMAGE:7123774 5', mRNA sequence.
CK479120
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmLOAOT Betheadd, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                 GATATGAAGGCCCTGATTCGAAACCGCAGCTACGTCTTCTCCTCCTCGCCACGTCGGCT
                                                                                      GIGICCCCTGGGCAIGAICACAGGAACACICAICCICATICTGGICCCAGCCACT
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Rattus norvegicus
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UI-M-HQO-cpf-d-17-0-UI.rl NIH_BMAP_HQO Mus musculus cDNA clone
IMAGE:30661624 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
I (bases 1 to 828)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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llarity 86.5%; Pred. No. 7.6e-111;
Conservative 0; Mismatches 105;
                                               1592 CTGCGCTCTTCGTCAGCGACCGCCAGG 1623
                                                                             CN528616
CN528616.1 GI:46856772
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Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMILIGS Tow: e column: 24

High quality sequence stop: 837.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                        BII59625 837 bp mRNA linear EST 05-JUL-2001 602920091F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5060351 5', mRNA sequence.
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/dev_stage="10 months"
/dev_stage="10 months"
/dev_stage="10 months"
/lab host="DH108"
/clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Öligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus Sukaryota, Chordata, Craniata, Vertebrata, Buteleostomi, Maukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Musl. (1 (bases 1 to 817) http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                          601 GCTGTGGCCTTGCAGAGCTTCACCTCCCCATCTGCTGGGGGGGACGCTGGAAGCCCCTACCTC
           GCCGTGGCCTTGCAGAGCTTCACCTCCCACCTGCTGGGGGACGCCGGGGAGCCCCTACCTC
                                                                                                                 1462 ATTGGCTTTATCTCAGACCTGATCCGCCAGAGCACTAAGGACTCCCCGGTCTGGG 1516
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Best Local Similarity 87.3%; Pred. No. 5.9e-103;
Matches 666; Conservative 0; Mismatches 92; Indels 5;
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                    /mol type="mrkha"
//db_xref="taxon:10116"
//db_xref="taxon:10116"
//clone="makks:7123774"
//tissue_type="lung, pooled"
//lab_hoEt="lung TonA"
//lab_hoEt="DH10B TonA"
//lab_hoEt="DH10B TonA"
//lab_hoEt="UNH MGC_221:
//note="Organ: lung; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled lung Tissues were
mix of male and female animals at 8 wk old. Tissues were
snap-frozen and kemale animals at 8 wk old. Tissues were
snap-frozen and wept at -80C for two days before RNA
extraction and purification (Tri-reagent method). CDNA was
primed using oligo-dT primer:
5. pGACTAGTTCTAGATCGGAGGGGCGCCCC(T) 25-3' and cloned into
the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 2.3 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC_211) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH_MGC library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM15012 row: e column: 20
High quality sequence stop: 692.
Location/Qualifiers
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Pred. No. 1.3e-106;
0; Mismatches 87;
                                                                                                                                                                                                                      organism="Rattus norvegicus"
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Pred. No. 6.5e-102;
0; Mismatches 482;
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Submitted (16-APR-2001) National Laboratory For Oncogenes & Related
Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, Shanghai
200032, P. R. China
Location/Qualifiers
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Losses 1 to 2144)
Zhou,X.M., Zhang,P.P., Jiang,H.Q., Huang,Y., Qin,W.X., Zhao,X.T.,
Wan,D.F. and Gu,J.R.
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Catarrhini; Hominidae; Homo.
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1 (bases 1 to 2144)

Huang, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao Wan, D.F. and Gu, J.R.

Novel human cDNA clones with function of inhibiting cancer
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/product="PP2030"
/protein_id="AAQ15259.1"
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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BE285645

1075 bp mRNA linear EST 26-OCT-2000 601097128F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3495966 5', mRNA sequence.

BE285645

BE285645.1 GI:9163408
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/dev_stage="pediatric 6 years"
/lab_host="DH108"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB.
GTCTCATCTTTGGACTCATCACCTGCCTGACCGGAGTCCTGGGTGTGGGCCTGGGTGTGG 1296
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1 (basea 1 to 53)

Wei, Y., Tasng, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr., Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F. Pediatric Leukemia CDNA Sequencing Project (2001)
Unpublished (2001)

Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                    1417 TGGCCACTTATATTTTCATCTTCATTGGAGAGCCCCCCCTGTCCATGAACTGGGCCATCG
                                                                                                                                                                                                                                                                                           AGATCAGCCGCCGGCTCCGCCACTCCAACCCCCGGGCTGATCCCCTGGTCTGTGCCACTG
                                                                                                                                                              TAGGAGCCTATATCTTCGTCGGGGAGACGCTGCTGTTTTCTAACTGGGCCATCA
                                                                                                                                                                                                                              1355 CTGCAGACATCCTCATGTACGTGGTCATCCCCACGCGGGGGGCGCCACTGCCGTGGCCTTGC
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                              GAGCCACGCGCTGGTGCCGCCTGAAGACCCAGCGGGCCGACCCACTGGTGTGTGCCGTGG
                                                                                                 GCATGCTGGGCTCTGCCATCTTCATCTGCCTGATCTTCGTGGCTGCCAAGAGCAGCATCG
                                                                                                                                                                                                                                                     1477 TGGCCGACATTCTGCTGTACGTGGTGATCCCTACCCGACGCTCCACCGCCGAGGCCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                1597 CTGACCGCCTGCGCCGGAACTGGCCCCCCTCCTTGTCCGAGTTCCGGGCTCTGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030,
Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="leukopheresis"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ter: 832-825-4038
Email: clones@txcc.org
Seq primer: M13 primer.
Location/Qualifiers
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Homo sapiens
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musina; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musina; Libaees 1 to 687)

32 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: Month of the Consortium/LLNL at:

Clone distribution: Month of the Consortium/LLNL at:

Http://mage.lln.gov

Plate: LLAM10327 row: i column: 10

High quality sequence stop: 650.

Location/Qualifiers
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/clone="IMAGE:4485585"
/tissue type="tumor, biopsy sample"
/tesue type="tumor, biopsy sample"
/dev sage="3 months, virgin"
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/clone=lbe="NCI_CGAP_Man1"
/note="Organ: mammarry, vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not!; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
481 TTTGTGGCTGCCAAGACCAGCATTGTAGGCGCTTATATCTGCATTTTTGTTGGAGAGACA
                                                                               1389 -GCGGCGCCCACTGCCGTGGCCTTGCAGGCTTCACCTCCCACCTGCTGGGGGACGCCG
                                                                                                                                                                              1448 GGAGCCCCTACCTCATTGGCTTTATCT-CAGACCTGATCCGCCAGAGCACTAAGGACTCC
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24.6%; Score 509.8; DB 4; Length 687;
Best Local Similarity 89.3%; Pred. No. 3.4e-93;
Matches 594; Conservative 0; Mismatches 67; Indels 4.
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/strain="FVB/N"
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musina 1 (1988)

I (Dasses It o. 1075)

IN IN-WGC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Localing Sequence stop: 624.

High quality sequence stop: 624.

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/ Organism="Mus musculus"

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CO401999 815 bp mRNA linear EST 01-JUL-2004
AGENCOURT 26753071 NIH MGC 255 Rattus norvegicus CDNA clone
IMAGE:7320138 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                  /clone_lib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Purther information about the clone and the sequencing project is availed at http://mipp.rgf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCTGTAGCTTCATGGCTGCCCCCATCTTCGGCTACCTGGGCGACCGCTTCAACAG
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                                                                                                                                                /organism="Pongo pygmaeus"
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/clone="bKF2p459J1933"
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Rattus norvegicus
                                                                                                                                                                                                                                                          /dev_stage="adult"
/lab_host="DH10B"
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pcorl) Pongo pygmaeus cDNA clone
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Pongo pygmaeus
Pongo pygmaeus
Pongo pygmaeus
Mawanjia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pongo.
1 (bases 1 to 524)
Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pongo, pygmaeus mRNA (Koehrer, K., Beyer, A., Mewes, H.W., et al.)
Unpublished (2004)
                                                                                                                          CTTTACGGGATTTCTGGGCGTGGTCACGGGGGGAGGCCACGCCTGGTGCCGCCTGAA
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AAACCGCAGTTACGTCTTCTCCTCCCTGGCCACATCCGCTGTGTCCTTCGCCACAGGGGC
                                                                CCTGGGCATGTGGATTCCCCTCTATCTTCACCGTGCTCAAGTTGTACAAAAGACAGCAGA
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DKFZp459J1933 rl 459 (synonym: p
DKFZp459J1933 s', mRNA sequence.
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AUTHORS
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/tissue_type="tumor, gross tissue"
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Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                         BG974364 172-JUN-2001
602844132F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4979959 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAM10978 row: p column: 08

High quality sequence stop: 719.
                                                                                                                                               540
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IH-MGC Http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/strain="NMRI"
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/clone="IMAGE:4979959"
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Mus musculus
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Conteat: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Betheda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin

College of Wisconsin (LIML)

Diagramation: MGC clone distribution information

Clone distribution: MGC clone distribution information

Clone distribution: MGC clone distribution information

Clone distribution: MGC clone distribution information

Plate: LiAM15381 row: o column: 16

High quality sequence stop: 672.
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Pred. No. 1e-91;
0; Mismatches 64; Indels 0

    .815
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="mRNA"
/db xref="taxon:10116"
/clone="IMAGE:7320138"
/sex="both"
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Best Local Similarity 89.4
Matches 541, Conservative
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      AUTHORS
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Rockville, MD 20850, USA  COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  FRATURES Location/Qualifiers 1. 1587   corganism="Homo sapiens"   /mol_type="genomic DNA"   /db_xref="taxon:9606"   /db_xref="taxon:9606"   /locus_tag="HCM1545"   /locus_tag="HCM1545"	Query Match 23.9%; Score 495.2; DB 9; Length 1587; Best Local Similarity 58.4%; Pred. No. 3.3e-90; Matches 799; Conservative 0; Mismatches 562; Indels 6; Gaps 2;	Qy 282 GGGCCCGGGCGCTCAGCAGCCCAAACCGGCCAGCTTGGGCCGGGGGGGG	OY 342 GGCGATCCTCAGCTTGGGCAACGTGCTCAACTACCTGGACAGGTACCGTGGCGGGGGT 401	QY 402 CCTTCTGGACATCCAGCAGCACTTTGGGGTCAAGGACCGAGCGGCCGGC	Qy         462         AGIGITCATCTGIAGCTTCATGATGGCTGCCCCCATCTTCGGCTACCTGGGCGACCGCTT         521           Db         306         CGIGITCATCTCCCAGTTACATGGTGTTGGCACCTGTGTTTGGCTACTGGGTGACAGGTA         365	OY 522 CAACAGGAAGGTGATTCTCAGCTGCGGCATTTTCTTCTGGTCGGCCGTCACCTTCTCCAG 581	QY         582         CTCCTTCATTCCCCAGCAGTACTTCTGGCTGCTCCTGTCCCGGGGCTGGTGGGCAT         641           Db         426         ATCCTTCATCCCCGGAGAGCATTTCTGGCTGCTCCTCCTGACCCGGGGCCTGGTGGGGGT         485	Qy 642 CGGGGGGCGGCTACTCCACCATGGCCCCCACTATCGTTGGCGACCTCTTCACCAAGAA 701	Qy         702 CACGCGTACGCTCATGCTGCTCTTCTACTTCGCCATCGCACTGGCCTGGG         761           Db         546 CAGCGGAGCCGATGCTCTCTTCTCTCCGTGGCAGTGGCCTGGG         605           CAGCGGAGCCGATGCTCTTCTTGCTTTGCTTCGGTGGCATCTGGG         605           Oy         762 CTACATTTGCTCGGCTGAGAGCATCTTGCCATTCGGTCTGGGCATTGAGGGT         665           Db         606 CTACATTGCAGGCTCCAAAGTGAAGGATATGGCTGGAGCTGGGCACTGAGGGT         665           Oy         822 GTCCCCTGTCCTGGGCATGATCACAGGAACTCATCCTCTTTGGTCCCACTGAGGCT         725           Db         666 GACACCGGGCTTAGGATCATCTGCTCATTCTGGTCCCACTCAGGCTCCCC         725           Oy         882 AAGGGGTCATGCGACCAGCACTCAGATTTCCCTCCTCTGTAGCTCCGCTCCTCATGGCTCCCC         726           Db         726 AAGGGGACCCTGACTTCAGATTTCCACTCCTCCTCCTCCTCGTCGTCGCTCGC
Oy         750         CAGTGGCCTACATTACTGGCTCCAGCGTGAAGCAGGCAGCGGAACTGGCACTG         809           Db         94         CAGTGGCCTGGGCTATTACTCAGCTTCCAGCGTGAAGCAGCTGGAGACTGCATTG         153           Oy         810         GGCATTGCGGGTGTCCCTG-TCCTGGCGTGATCACAGGAACACTCATCTGG         868           Db         154         GGCCTGGGGGTTTCCCCGGATCCTGGGGATCATGATCACAGGAACACTCATCCTCATCTTGG         213           Oy         869         TCCCAGCCACTAAAAAGGGGCATGCTGATGATCACAGGACCAGCTCAAGGCCCGACCT         228           Db         214         TCCCAGCCACTAAAGAGGCATGATCAACTAACTGAGGCCCAAGCTCAAAGCACGACCT         23	Oy 929 CATGGCTCCGAGATATGAAGGCCCTGATTCGAAACCGCAGCTACGTCTTCTCCTCCTGG 988	Ay 989 CCACGTCGGCTGTCCTTCGCCACGGGGCCCTGGGCATGTGGATCCGGTCTACCTGC 1048	OY 1049 ACCGCCCCAAGTTGTGCAGAAGACAGCAGAGCGCGCCCCGCCCTGTGGGGCCA 1108	0y 1109 AGGACAGCCTCATCTTTGGGGCCATCACCTGGTTTACGGGATTTCTGGGCGTGGTCACGG 1168	Oy         1169         GGGCAGGAGCACGCG-CTGGTGCCCTGAAGACCCAGCGGGCCGACCCATGGTGT         1227           Db         514         GCGCGGGAGCCACTCGATTGGTGCCCTGCGGACTCAACGTGCTGACCCATAGGTGTGT         573	Qy 1228 GCCGTGGGCATGCTGGCCTTCTTCATCTGCCTGATCTTCGTGGCTGCCAAGAGC 1287	OY 1288 AGCATCGTAGGAGCCTATATCTGTATCTTCGTCGGGAGACGCTGCTGTTTTCTAACTGG 1347	Qy         1348         GCCATCACTGCAGACATCCTCATGTACGTG         1377           Db         694         GCCATCACTGCAGACATCCTCATGTATGTG         723	RESULT 14 AY403401 LOCUS DEFINITION No sapiens HCM1545 gene, VIRTUAL TRANSCRIPT, partial sequence, accession AY403401 AYA03401 ASS. SOURCE ORGANISM Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo. Inflaction sapiens AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Du, F., Murphy, B., Adams, M.D. and Cargill, M. TITLE AUTHORS Clark, G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Adams, M.D. and Cargill, M. AUTHORS Clark, G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., TATLE AUTHORS Clark, G., Glanowski, S., Nielson, R., Du, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. TITLE Direct Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

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CCGTGGGCATGCTGCCATCTTCATCTGCCTGATCTTCGTGGCTGCCAAGAGCA 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="NIA:A0840B03 IMAGB:30761006"
/tissue_type="whole embryo including extraembryonic tissues at 13.5-days postcoitum"
/dev stage="E13.5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.3%; Score 483; DB 7; Length 579;
89.6%; Pred. No. 9.6e-88;
tive 0; Mismatches 60; Indels
   xref="niaEST:A0840B03-5"
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Musmamalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 579)

2 Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,

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Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A.,

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D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

Transcriptome analysis of mouse stem cells and early embryos

L. Docacci Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

Sind Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov
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TCTCATCTTTGGACTCATCACCTGCCTGACCGGAGTCCTGGGTGTGGGCCTGGGTGTGGA 1025
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/mol_type="mRNA"
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Human, NOVX, atherosclerosis, hypertension, obesity, cancer, cytostatic, hypotensive, antiarteriosclerotic, anorectic, gene therapy, NOV19, spinster-like protein, chromosome 17.
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                                    ADI23111
ABB52112
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ADI2370
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20010S-0272404P.
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ADH48764;
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Ade04896 Human tra
Ade08326 Novel pro
Adm38697 Human 464
Add37478 Human 464
Add1327 Human 464
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Ad057285 Kidney de
Am40483 Human pro
Abb023616 Human pro
Aae06616 Human pro
Aae06616 Human pro
Aae16786 Human tra
Ade1899 Human tra
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Human
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Compugen Ltd
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Copyright (c) 1993 - 2004
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Listing first 45 summaries
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AAM38697
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Gapop 10.0 , Gapext 0.5
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Burford N,
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                                                                                                                                                                                                                                                                                                                                         any number from 1 to 91 and their coding sequences. The proteins and coding sequences are useful for preventing or treating disorders or syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV19 a spinster-like protein and its coding sequence maps to chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAGSPYLIG
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                                                                                                           Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE; Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA; Gorman L, Guo X, Gusev VY, Kekuda R, Li L, Liu X, Malyankar UM; Miller CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Peyman J Kastelli L, Shenoy SG, Shimkets RA, Smithson G, Spytek KA, Stone Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MMCLECASAAAGGAEEEEADAERRRRRGAQRGAGGSGCCGARGAGGAGVSAAGDEVQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                               The present invention relates to novel human NOVX proteins, where X
                                                                                                                                                                                                                                                New NOVX polypeptides or polynucleotides, useful for preventing or treating disorders or syndromes e.g., atherosclerosis, hypertension,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2920; DB 5;
100.0%; Pred. No. 5.2e-255;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                       Claim 1; Page 130; 923pp; English.
     16-AUG-2001; 2001US-0312858P.
17-AUG-2001; 2001US-031280P.
29-AUG-2001; 2001US-0315614P.
17-SEP-2001; 2001US-0322818P.
25-FEB-2002; 2002US-00322818.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 566; Conservative
                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                            WPI; 2002-698672/75.
                                                                                                                                                                                                                                                                               obesity or cancer.
                                                                                                                                                                                                                         N-PSDB; ADH48763
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Human; transporter and ion channel-9; TRICH-9; vaccine; cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; aethma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; mood; arrhythmia; pick's disease; lschaemic cerebrovascular disease; ALDS; anxiety; stroke; Huntington's disease; Parkinson's disease; Cerebral neoplasm; allergy; dementianting disease; mental disorder; Schizophrenia; polymyositis; disease; deractiomyopathy; cataract; myocarditis; grave's disease; theumatoid arthritis; Sjogren's syndrome; systemic lugus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery seenosis; nootropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is transporter and ion channel-9 (TRICH-9) protein. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, buchenne muscular dystrophy, and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischaemic cerebrovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reddy R;
Gandhi AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human transporter and ion channel proteins useful for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing transport, neurological, muscle and immunological disorders.
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imzai Y, Yue H, Nguyen DB, Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                 Human transporter and ion channel-9 (TRICH-9) protein.
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/label= Transmembrane_domain
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566
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                                                                                                                                                                                   AAE04896 standard; protein; 398
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14-JAN-2000; 2000US-0176883P.
21-JAN-2000; 2000US-0177332P.
28-JAN-2000; 2000US-0179758P.
02-FBE-2000; 2000US-0179758P.
10-FEB-2000; 2000US-0181625P.
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/label= Tra:
350.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                        of the invention.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 312 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stroke, cerebral neoplasms, Pick's disease, Huntington's disease and mod, arxiety, Schlzophrenia and seasonal affective disorder; muscle disorder including mod, arxiety, Schlzophrenia and seasonal affective disorder; muscle disorder including cardiomyopathy, myocarditis, polymyositis, dernythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma; Siggran's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
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                                                                                                                                                                                                                                                                    1 MVAAPIFGYLGDRFNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYS
                                                                                                                                                                                                                                                                                                                   61 TIAPTIIGDLFTKNTRTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGM
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                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                     Score 1978; DB 4; Length 398;
Pred. No. 5.3e-170;
2; Mismatches 2; Indels (
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Best Local Similarity 99.0%;
Matches 384; Conservative 2
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11-DEC-2001; 2001US-0339453P.
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                                                                                                                                                                                  Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides, useful for expressing recombinant proteins fanalysis, characterization or therapeutic use, or as markers for in which the corresponding protein is preferentially expressed.
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ou P, Drmanac RT,
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Pred. No. 2.6e-136;
0; Mismatches 1;
                                                                                                                                                                                                                                                       W, Ren F, Zhang
Weng G, Zhou P,
Boyle BJ;
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                                                                                                                                                                                                                                                 Tang YT, Asundi V, Goodrich R
Ghosh M, Xue AJ, Wehrman T,
Ma Y, Wang D, Chen R, Xu C,
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-037281P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-00128558.
24-APR-2002; 2002US-00128558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.7%;
Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-569235/53.
N-PSDB; ADE07415.
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522

361 462

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Human; transporter protein; anorectic; antidiabetic; anti-Parkinsonian; nootropic; neuroprotective; hypotensive; antidepressant; neuroleptic; cardiovascular; immunosuppressive; gene therapy; sugar homeostasis; obesity; diabetes; anorexia; central nervous system disorder; depression; CNS disorder; Parkinson's disease; Alzheimer's disease; hypertension; autonomic function disorder; schizophrenia; learning disorder; amnesia; memory disorder; age-related disorder; cardiovascular disorder; isonemicy; restenosis; hormonal disorder; creperfusion injury; restenosis; hormonal disorder; chronic mucocutaneous candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                The present sequence represents the human 46455 protein, which is a member of the transporter family. The transporter family proteins (I)
DQRSRMLSIFYFAIPVGSGLGYIAGSKVKDWAGDWHWALRVTPGLGVVAVLLLFLVVREP
                                                                                                        242 PRGAVERHSDLPPLNPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLLRS
                                                                                                                                                   QVVQKTAETC-NSPPCGAKDSLIFGALTCFTGFLGVVTGAGATRWCRLKTQRADPLVCAV
                                                                                                                                                                                           RVVLGETPPCLPGDSCSSSDSLIFGLÍTCLTGVLGVGLGVEISRRLRHSNPRADPLVCAT
                                                                                                                                                                                                                                                                QSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLAT
                                                                285 KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA
                                                                                                                                                                                                                                          GMLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALFFVSDRARAEQHLGE--RRAGVR----VVHQRG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 46455 transporter protein SEQ ID NO:5.
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18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
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N-PSDB; ABQ74262, ABQ74263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 NTRILMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILLVPAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AGDEVQTLSGSVRRAPTGP-PGTPGCAATAKGPGAQOPKPASLGR-----GRGA-A 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ě
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vel nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang D;
Zhao Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGSDTAPPLSQADDPDDGPVPGTPGLPGSTGNPKSEEPBVPDQEGLQRITGLSPGRSALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Gaps
               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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44.5%; Score 1298; DB 4;
Best Local Similarity 53.4%; Pred. No. 2.4e-108;
Matches 275; Conservative 62; Mismatches 162;
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Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 1842; 10078pp; English.
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
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03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
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                                                                                                                                                                                             WO200153312-A1.
                                                                                                                                                     Homo sapiens.
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                                                                                                           leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang J,
Zhou P,
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Human, transporter, cytostatic, anorectic, antidiabetic, anticonvulsant, gene therapy, PGC-1 associated disorder, liver tumour, obesity, epilepsy,

(first entry)

15-JAN-2004

Human transporter 46455.

US2003143675-A1.

Homo sapiens.

gene ther diabetes.

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The production of the control of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.5%; Score 1298; DB 5; Length 528;
53.4%; Pred. No. 2.4e-108;
ive 62; Mismatches 162; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune disorders (e.g. chronic mucocutaneous candidiasis)
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Best Local Similarity 53.4%
Matches 275; Conservative
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285 KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
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165 FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 QVVQKTAETC-NSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAV 402
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482

RESULT 6

ADD37478 standard; protein; 528

ADD37478

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The invention relates to an isolated nucleic acid comprising a cDNA encoding a human transporter protein, or its complement, a sequence that is 60 % identical to the cDNA, a fragment comprising at least 30 nucleotides of the cDNA, or a sequence encoding a fragment of the cDNA. Also included are a vector comprising the novel nucleic acid condecule, producing the polypoptide, the isolated transporter collypeptide, an isolated antibody that specifically binds to the collypeptide, an isolated antibody that specifically binds to the collypeptide, detecting the presence of the polypoptide or nucleic acid in a sample, a kit, identifying a compound that binds to, or that modulates the activity of the polypoptide, and adulating the activity of the collypeptide. The nucleic acid is useful for preparing a composition for treating PGC-1 (not defined) associated disorders e.g. liver tumours, observed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy
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                                                                                                                                                                                                                                                                                                      2000US-0248364P.
2000US-0248878P.
2000US-0256588P.
2000US-0256588P.
2000US-0256588P.
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2001US-00895811.
2001US-00919781.
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21-DEC-2000; 2
22-JAN-2001; 2
14-MAY-2001; 2
29-JUN-2001; 2
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25-SEP-2000; 2
05-OCT-2000; 2
14-NOV-2000; 2
15-NOV-2000; 2
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164
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                                                                                                                                                                                                                                GMLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVAL 462
AGDEVQTLSGSVRRAPTGP-PGTPGTPGCAATAKGPGAQQPKPASLGR-----GRGA-A 104
                                                61
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Alzhaimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                             QSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLAT
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AIFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRG
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2000US-0195734P.
2000US-0195939P.
2000US-019593P.
2000US-013537P.
2000US-0235018P.
2000US-0235018P.
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2000US-0256588P.
2000US-0258028P.
2001US-00796720.
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03-MAR-2000;
07-APR-2000;
11-APR-2000;
26-APR-2000;
19-SEP-2000;
25-SEP-2000;
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21-DEC-2000;
28-PEB-2001;
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The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,

CC IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

CC IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 Icm Clearing to acids and proteins. The TWIK-6, TWIK-7, IC23927,

TWIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC TWIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC Gamosing and treating ICF-related diseases. The sequences may be used

CC diagnosing and treating ICF-related diseases. The sequences may be used

CC diagnosing and treating ICF-related with decreased expression by rectifying

CC mutations or deletions in a patient's genome that affect the activity of

CC ICF proteins by expressing inactive proteins may be used as

CC antigens in the production of antibodies against ICF proteins and in

CC antigens in the production of antibodies against ICF proteins and in

CC antigens in the production of antibodies against ICF proteins and in

CC antigens in the production of antibodies against ICF proteins and activity. The

CC antilICF protein antibodies, agonists and antagonists may be used to

CC regulate ICF protein expression and activity. The antibodies may also be

CC samples (e.g. by immunosasay). The nucleic acids and proteins may be used

CC samples (e.g. by immunosasay). The nucleic acids and proteins may be used

CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple

CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple

CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple

CC sequence represents the human 46455 protein of the invention. Note: The

CC USFTO at sequence is also available in electronic format from

CC USFTO at sequence huml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AGDEVQTLSGSVRRAPTGP-PGTPGTPGCAATAKGPGAQQPKPASLGR-----GRGA-A 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 PRGAVERHSDLPPLNPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLLRS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1298; DB 8;
Pred. No. 2.4e-108;
                                                                                                                                                                                                                       Silos-Santiago
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 50; 638pp; English.
2001US-00828035.
2001US-00833081.
2001US-00843128.
2001US-00957683.
2001US-00964255.
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Best Local Similarity 53.4%;
Matches 275; Conservative 62
                                                                                                                                                                                                                       RAJ, Glucksmann MA,
                                                                                                                                   2001US-00024623
                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
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Best Local Similarity
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06-APR-2001; 2
11-APR-2001; 2
25-APR-2001; 2
19-SEP-2001; 2
25-SEP-2001; 2
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                                                      421
                                                                                                            481
RVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEISRRLRHSNPRADPLVCAT 361
                                                                                                                                                                                                                                                                                                                                                 predictor set; protein tyrosine kinase; cytostatic; antiangiogenic; vasotropic; vulnerary; pharmacogenomic; drug sensitivity; breast cancer; hypervascular disease; angiogenesis; wound healing scar; human; biomarker; spinster-like.
                          GMLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVAL
                                           QSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLAT
                                                                                                  New predictor sets with a plurality of polynucleotides and/or polypeptides whose expression pattern predicts cell response to a compound that modulates protein tyrosine kinase activity, useful in
                                                                                                                                                                                                                                                                                                                           Human protein tyrosine kinase biomarker spinster-like protein.
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44.5%; Score 1298; DB 8; Best Local Similarity 53.4%; Pred. No. 2.4e-108; Matches 275; Conservative 62; Mismatches 162;
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                                                                                                                                                                  482 AIFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRG 516
                                                                                                                                        ALFFVSDRARAEQHLGE--RRAGVR----VVHQRG
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                                                                                                    FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
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                                                                                                                    225 NTRTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILLLVPAT
                                                                                                                                                                            QIVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGT
                                           105 AAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDR
                                                              285 KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA
                                                                                                                                                                                                                                                  242 PRGAVERHSDLPPLNPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLLRS
                                                                                                                                                                                                                                                                               QVVQKTAETC-NSPPCGAKDSLIFGALTCFTGFLGVVTGAGATRWCRLKTQRADPLVCAV
                                                                                                                                                                                                                                                                                                                                       GMLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVAL
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| AIFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRG 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2002; 2002US-0368760P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopkins N, Golling G,
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GOLLING G.
AMSTERDAM A.
SUN Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-304692/28.
N-PSDB; ADO57284.
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AGDEVQTLSGSVRRAPTGP-PGTPGTPGCAATAKGPGAQQPKPASLGR-----GRGA-A 104

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7;

Indels 16; Gaps

peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

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The invention describes an isolated nucleic acid molecule (I) comprising a sequence of 1808 base pairs (1800 ID NO: 59) given in the specification, cover at least 600 contiguous base pairs, where the nucleic acid functions in kidney development. (I) is useful for treating or preventing a kidney disorder in an organism, where the nucleic acid elicitis an alteration in expression of a 459 nucleic acid sequence in the organism and compositions or prevents a side elicitis an alteration in expression of a 459 nucleic acid sequence in the organism and composition or also be used in dispnosing, preventing and treating a variety of mammalian diseases and developmental disorder. The nucleic acid may disorders, hearing disorders, hearing disorders, hearing disorders, proliferative disorders, or bone defects or disorders as well as in screening for compounds that modulate the development of an organism as a whole or of specific tissues or organs within that organism. This is the amino acid sequence of a kidney
New 459 nucleic acids and encoded polypeptides, useful for diagnosing, treating or preventing a kidney disorder in an organism, or in screening for compounds that modulate the development of an organism.
                                                                                                                 Disclosure; SEQ ID NO 52; 347pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development associated protein
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                                                                                                                                                                                                                   SAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFT 466
                                                                                                                                                                                                                                                            RKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNT 226
                                                                                                                                                               GHADQLGDQLKARTSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVV 346
                                                                                                                                                                                                       347 QKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLG 406
                                                                                                                                                                          107 ILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFN
                                                                                                                                     RTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKR
                     Gaps
                    3;
 DB 8; Length 507;
                     Indels
43.0%; Score 1256.5; DB 8; 56.4%; Pred. No. 1.3e-104; ive 66; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                              VSDRARAEQHLGERRAGVRVVHQRG 551
                      Conservative
          Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                                                                                                 527
                                                                                 167
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  Query Match
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wang D; , Zhao Q

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Ren F, Zhang

Qian XB, Yang Y,

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undi V, Chen R, hrman T, Xu C, 1 Drmanac RT;

Asundi V, Wehrman T,

Liu C, Asun Wang Z, Wehr Goodrich R,

Tang YT, ب ب ب

Zhou Wang

2001-442253/47.

N-PSDB; AAI59639

990S-00471275. 2000US-00488725. 2000US-0055317. 2000US-00598042.

21-JAN-2000; 25-APR-2000; 20-JUN-2000; 19-JUL-2000;

23-DEC-1999;

26-DEC-2000; 2000WO-US034263

WO200153312-A1

26-JUL-2001

Homo sapiens.

leukaemia.

2000US-00653450. 2000US-00662191. 2000US-00693036.

2000US-00727344

19-OCT-2000; 29-NOV-2000;

14-SEP-2000; 03-AUG-2000;

(HYSE-) HYSEQ INC.

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic.

Immunosuppressant and cyrostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries peripheral nervous fortal nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, asseasys for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 APTGPPGT---PGTP-----GCAATAKGPGAQQPKPASLGRGRGAAAAILSLGNVLNYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 RYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 SAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNTRTLMLSVFYFAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 TGARAGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 SAAAGGAEEEEEADAERRRRRGAQRGAGGSG-CCGARGAGGAGVSAAGDEVQTLSGSVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1250; DB 4;
Pred. No. 6e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 5414; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
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Best Local Similarity 50.9<sup>1</sup>
Matches 268; Conservative
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

Human polypeptide SEQ ID NO 5414.

(first entry)

22-OCT-2001

AAM40483;

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AAM40483 standard; protein; 581

RESULT 10 AAM40483

Crohn's disease,

us-10-085-198-48.rag

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multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) caradiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
     autoimmune thyroiditis, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB23610 standard; protein; 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                  al Similarity 56.7
251; Conservative
                                                                                                                              Sequence 455 AA;
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Best Local
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                                                                                               R-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETC-NSP 356
                                                                                                                          411
                                                                                                                                                    PCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV 416
                                                                                                                                                                                                           476
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                                                                       351
                                                                                                                                                                             412 SCSSSDSLIFGLITCLTGVLGVGLGVEISRRLRHSNPRADPLVCATGLLGSAPFLFLSLA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
PLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKRGHADQLGDQLKA
                                                                                                               AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                523
                                                                                                                                                                                                                                                                                          578
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                                                                                                                                                                                                                                                             YLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATA
                                                                                                                                                                                                                                                                                532 YLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 2641.
                                                                                                                                                                                                                                                                                                                                                             ABB90265 standard; protein; 455
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N-PSDB; ABL90674.
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                                                                                               299
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                                                                                                    301 LACARGSIVATYIFIFIGETLLSMWWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATALFFVSDRARAE
                                                                                117 LDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIF
                                                                                                                                                            FWSAVIFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNTRTLMLSVFYP
                                                                                                                                                                                AIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILLVPATKRGHADQLGDQL
                                                                                                                                                                                                                                                                                                                      KAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTABTC-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAG
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; cytokine; cell proliferation;
nutritional supplement; immune modulation; autoimmune disorder;
haematopoiesis regulation; tissue growth; haemostasis; inflammation.
                                           .;
8
Length 455;
                                         Indels
  41.8%; Score 1222; DB 5; 1
56.7%; Pred. No. 1.5e-101;
iive 58; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11. .23
/label= signal_peptide
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/label= mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein SEQ ID NO: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                           The present sequence is the sequence of a human secreted protein. Its coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic activity, or anti-
                                                                                                                                                                                                             which are
and research, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, hydrophobic domain, gene therapy, nutritional supplement,
cell proliferation, immunomodulatory, autoimmune disorder, antimicrobial,
multiple sclerosis, rheumatoid arthritis, insulin-dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 MKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETCNSPPCGAKDSLI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKSSIVGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YICIFVGETLIFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAGSPYLIGFISDL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKSSIVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YICIFVGETLLFSNWAITADILMYVVIPTRRATAVALOSFTSHLLGDAGSPYLIGFISDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETCNSPPCGAKDSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IROSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATALFFVSDRARAEQHLGE 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 244;
                                                                                                                                                                                                             secreted proteins and polynucleotides encoding them, ived from Homosapiens, useful for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                        Rapiejko P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein having hydrophobic domain, HP10735.
                                                                                                                                                                                                                                                                                                                                                                                                                                     40.3%; Score 1176; DB 3;
97.9%; Pred. No. 9.8e-98;
ive 2; Mismatches 3;
                                                                                                                                                        Hall J,
                                                                                                                                                                                                                                    well as nutritional sources or supplements
                                                                                                                                                                                                                                                         Claim 29; Page 254; 309pp; English.
                                                                                                                                                        Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE06616 standard; protein; 476
                             99US-0120680P.
99US-00298733.
99US-0149639P.
99US-0155686P.
99US-0157247P.
                                                                                                 29-NOV-1999; 99US-0167823P.
15-FEB-2000; 2000US-0182711P.
          2000WO-US004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                      Valenzuela D, Yuan O,
                                                                                                                                 (ALPH-) ALPHAGENE INC
                                                                                                                                                                                                                                                                                                                                                                                            inflammatory activity
                                                                                                                                                                              WPI; 2000-549267/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                       N-PSDB; AAA93110
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 244 AA;
          18-FEB-2000;
                                          23-APR-1999;
17-AUG-1999;
23-SEP-1999;
                                                                         01-OCT-1999
29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Simi
Matches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366
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The present sequence is named polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with prevention, diagnosis and treatment of diseases associated with correct the polypeptide expression. The polypucleotides may be used to produce the polypeptide, by inserting the mucleic acids into a host cell complementery sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify as antigens in the production of antibodies and in assays to identify concluder of polypeptide expression and activity. The polypeptides and mucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autonimume disorders such as multiple sclerosis, rheumatoid architic and inside growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate activin and chemokantic and chemokantic activity, to modulate activity chemokantic and chemokantic activity, to modulate activity controlling fertility activity (e.g. for controlling fertility) and activity (e.g. for controlling fertility).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 AGDEVQTLSGSVRRAPTGP-PGTPGCAATAKGPGAQQPKPASLGR-----GRGA-A 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
haematopoiesis, tissue growth activity, Parkinson's disease, cytostatic, multington's disease, Alzheimer's disease, chemotactic, chemokinetic; haemostatic, thrombolytic, tumour growth inhibitor; anabolic; contraceptive, antiinfertility, antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is human protein with hydrophobic domain, HP10735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEEPEVPDQEGLQRITGLSPGRSALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 150-151; 563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000; 2000JP-0000585.
06-JAN-2000; 2000JP-0000589.
11-JAN-2000; 2000JP-0002299.
03-FEB-2000; 2000JP-0056865.
03-MAR-2000; 2000JP-00058857.
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(SAGA ) SAGAMI CHEM RES CENT.
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gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy, hypertension; angina; neurological disorder; aethma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; Pick's disease; ischaemic cerebrovascular disease; AlbS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer.
                                                                                                                         403
                                                                                                                                                                                      463
                                                                                                                                                                                                        371 IVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGTA 430
NTRTLALSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPAT 284
                 KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
                                                                                                                                                      ------LIFGLITCLTGVLGVGLGVEISRRLRHSNPRADPLVCATG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transporter and ion channel-12; TRICH-12; cystic fibrosis; mood;
                                                                                                                         QVVQKTABICNSPPCGAKDSLIFGAIICFIGFLGVVTGAGATRWCRLKTQRADPLVCAVG
                                                                                                                                                                                   404 MLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQ
                                                                                                                                                                                                                                                  SFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human transporter and ion channel-12 (TRICH-12) protein.
                                                                                                                                                                                                                                                                                                                551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222. .239
/label= Transmembrane_domain
327. .350
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/label= Transmembrane_domain
413. .432
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                             LFFVSDRARAEQHLGE--RRAGVR----VVHQRG
                                                                                                                                                                                                                                                                                                                                                                                                                        AAE04899 standard; protein; 476
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2000US-0177332P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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2000US-0178572P 2000US-0179758P 2000US-0181625P

28-JAN-2000; 02-FEB-2000; 10-FEB-2000;

(INCY-) INCYTE GENOMICS INC.

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control as transport disorder including amyotrophic lateral sclerosis, cachesase, buchenne muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, cachesase, Duchenne muscular dystrophy, angina and hypertension, cachesase, Duchenne muscular dystrophy, ischaemic cerebrovascular disease, dementia, depression, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease, and Parkinson's disease, demyelinating diseases, mental disorders and Parkinson's disease, demyelinating diseases, manched disorder including cardiomyopathy, myocarditis, polymyositis, carribythmias and astwa and immunological disorders including arbitis, arribythmias and astwa and immunological disorders including arbitis, scleroderms, Sjogren's canemia, diabetes mellitus, rheumatosus and other diseases including respiratory distress syndrome, systemic lupus erythematosus and other diseases including.

Constitution dispersion of disease, cataracte, infertility, pulmonary sickle cell anaemia, Wilson's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AGDEVQTLSGSVRRAPTGP-PGTPGCAATAKGPGAQQPKPASLGR-----GRGA-A 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 VAVLCYINLINYMDRFTVAGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 QVVQKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 IVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGTA 430
                                                                                                                                                                                  Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEBPEVPDQEGLQRITGLSPGRSALI 61
                     N, Au-Young J, Lu DAM, Yang J, Reddy R;
Azimzai Y, Yue H, Nguyen DB, Yao MG, Gandhi AR;
                                                                                                                                                                                                                                                                                                  The present sequence is transporter and ion channel-12 (TRICH-12) protein. TRICH is used as vaccine. TRICH is useful for treating a dise or condition associated with decreased expression of functional TRICH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 PRGAVERHSDLPPINPTSWWADLRALARN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 ------Lirgilitchidolgveiskelehsnpradplocate
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49.4%; Pred. No. 1.5e-96;
                                                                                                                                                                                                                                                      Claim 1; Page 124-125; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 254; Conservative
                     Baughn MR, Burford N,
Lal P, Hillman JL, A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                           WPI; 2001-418042/44
N-PSDB; AAD09563.
                                                               Tang YT, Khan FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 476 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449
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38.2%; Score 1115; DB 7; Length 420;
Best Local Similarity 56.6%; Pred. No. 6.4e-92;
Matches 231; Conservative 50; Mismatches 119; Indels
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IFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRG 464
           LFFVSDRARAEQHLGE--RRAGVR----VVHQRG 551
                                                                                                                                                                                                Human cancer suppressor protein PP2030,
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                                                                                                          ADLO8448 standard; protein; 420
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Search completed: October 23, 2004, 13:12:09 Job time: 93 secs

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Sequence 396, App
Sequence 555, App
Sequence 554, App
Sequence 30568, Ap
Sequence 13997, A
Sequence 46, Appl
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Sequence 7567, Ap
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Sequence 25053, A
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Sequence 10457
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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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## ALIGNMENTS

Sequence 396, Application US/09149476
Patent No. 6420526
GENERAL REPREMENTED:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFRENCE: P2002P1
CURENT APPLICATION NUMBER: US/09/149,476
CURENT APPLICATION NUMBER: US/09/149,476
CURENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 591
EARLIER PILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23

ERRLIER APPLICATION NUMBER: 60/047,500
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ERRLIER FILING DATE: 1997-06-31
ERRLIER FILING DATE: 1997-04-13-38
ERRLIER FILING DATE: 1997-06-22
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ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/043,578
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
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ER APPLICATION NUMBER: 60/047,501
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ER FILING DATE: 1997-06-22
ER APPLICATION NUMBER: 60/056,632
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,664
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R FILING DATE: 1997-08-22

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R FILING DATE: 1997-05-23

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APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884
FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 EARLIER APPLICATION NUMBER: 60/056,862 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,887 EARLIER FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,908 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22
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R FILING DATE: 1997-04-11

R PILING DATE: 1997-04-11

R PILING DATE: 1997-04-11

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PPLICATION NUMBER: 60/047,587
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FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                   Length 299
                                                                                                                                                                                                                                                                                                                                       91; Indels
                                                                                                                                                                                                                                                            26.7%; Score 779; DB 4;
56.1%; Pred. No. 1.5e-61;
tive 34; Mismatches 91
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ0022P1
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CURRENT PELING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US/09/149,476
EARLIER PELING DATE: 1998-03-06
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PELING DATE: 1997-03-07
EARLIER PELING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,533
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/047,597
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
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Patent No. 6420526
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Best Local Similarity
Matches 162; Conserv
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EARLIER PELICATION NUMBER: 60/056,913
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,913
EARLIER APPLICATION NUMBER: 60/056,913
EARLIER APPLICATION NUMBER: 60/056,914
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EARLIER APPLICATION NUMBER: 60/056,914
EARLIER PILING DATE: 1997-08-22
EARLIER PELICATION NUMBER: 60/056,845
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EARLIER PELICATION NUMBER: 60/056,945
EARLIER PELICATION NUMBER: 60/047,595
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EARLIER PELICATION NUMBER: 60/047,595
EARLIER PILING DATE: 1997-08-23
EARLIER PELING DATE: 1997-08-23
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433 373 256 AGDWHWALRVSPVIGMITGTLILLIVPATKRGHADQLGDQLKAR-TSWLRDWKALIRNRS 374 GFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKSSIVGAYICIFVGE Gaps 7 Query Match
23.0%; Score 672; DB 4; Length 424;
Best Local Similarity 54.0%; Pred. No. 9.1e-52;
Matches 142; Conservative 32; Mismatches 87; Indels APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILER REFERENCE: PZOOZPI
CURRENT PEDELICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: CO/040,162
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23 EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-05
EARLIER PELICATION NUMBER: 60/057,650
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-08-05
EARLIER FILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER FILING DATE: 1997-06-13 516 242 FLSEFRALQFSLMLCAFVGALGG 264 Sequence 554, Application US/09149476 Patent No. 6420526 GENERAL INFORMATION: 494 PLWEFLSLGYALMLCPFVVVLGG RESULT 3 US-09-149-476-554 셤 음 à 셤 ð 셤 g Š ઠે

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NUMBER: 60/047,502 1997-05-23 NUMBER: 60/047,633 1907-05-23 NUMBER: 60/047,583 1997-05-23 NUMBER: 60/047,617 1997-05-23 NUMBER: 60/047,618 1997-05-23 NUMBER: 60/047,592 NUMBER: 60/047,503 1997-05-23	23. 60/047, 58 20. 60/047, 58 20. 60/047, 58 20. 60/047, 58 20. 60/047, 49 20. 60/047, 59 20. 60/047, 59 20. 60/047, 59 20. 60/047, 61 20. 60/047, 61 20. 60/047, 61 20. 60/047, 61 20. 60/047, 61 20. 60/047, 61 20. 60/043, 58 20. 60/043, 58	NUMBER: 60/043,311. NUMBER: 60/043,671 1997-04-11 NUMBER: 60/043,674 1997-04-11 NUMBER: 60/043,132 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,315 1997-04-11 NUMBER: 60/049,315 1997-04-11 NUMBER: 60/049,315 1997-06-06 NUMBER: 60/056,886 1997-08-22 NUMBER: 60/056,889 1997-08-22 NUMBER: 60/056,899 1997-08-22 NUMBER: 60/056,893 1997-08-22 NUMBER: 60/056,893
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BARLIER PILLING DATE: 1997-08-22

BARLIER PILLICATION NUMBER: 60/056, 812

BARLIER PAPLICATION NUMBER: 60/056, 813

BARLIER PAPLICATION NUMBER: 60/056, 819

BARLIER PILLING DATE: 1997-08-22

BARLIER PILLING DATE: 1997-08-23

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107146.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR APPLICATION NUMBER: US 60/094,190
RIOR APPLICATION NUMBER: US 60/094,190
RIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30568
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440 W--AITADILMYVVIPTRRATAVALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWE 497
                                                                                                                                                                                                                                                                                                                              165 GHVGVVYGSIVAVFGCLGIVFGGRLADYWA--KRGRSDANM-RVGLL--AAWAVIPF---
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                                                                              327 FATGALGMWIP-LYLHRAQVVQKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGAT
                                                                                                                  268 MALYSLISWIPAFYIRKFQLAP-----TETGYWLGTILLVANTLGVFCAGWLN
                                                                                                                                                                                  386 RWCRLKTQRADPLVCAV-GMLGSAIFICLIFVAAKSSIVGAYICIFVGETLL----FSN
                                                                                                                                                                                                                    194 WLLVLSRGLVGIGEASYSTIAPTIIGDLFTKWTRTLMLSVFYFAIPLGSGLGYITGSSV-
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; Patent No. 6551795
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Best Local Similarity
Matches 87; Conserv
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US-09-252-991A-30568
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ORGANISM:
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Sequence 7272, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-019A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PALLICATION DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 LDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSV-FICSFMVAAPIFGYLGDRFNRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- AAGDWHWALRVSPVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%; Score 396; DB 4; Length 136;
65.2%; Pred. No. 9.5e-28;
ive 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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        EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-08-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
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US-09-328-352-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.2'
Matches 73; Conservative
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US-09-328-352-7272
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95 ASLGRG-----RGAAAAILSLGNVLNYLDRY---TVAGVLLDIQQHFGVKDRGAGLLQS 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 GDQLKA------RTSWLRDMKALIRN--RSYVFSSLATSAVSFATGALGMWIPL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 IQEIKAELEATVSEEKAGKASWGELFRGRTRPKVRQRLLMGVMLQAFQQLTG-----INA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AALGGGFLFGYDTGVIGGFLAL -- IDFLFRFGLLTSSGALAEL -- VGYSTVLTGLVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.9%; Score 202.5; DB 4; Length 488; Best Local Similarity 21.5%; Pred. No. 1.2e-09; Matches 114; Conservative 88; Mismatches 195; Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 YLHRAQVVQKTAETCNSPPCGAKDSLIFGAITCFTGFLGVV------
                PRIOR APPLICATION NUMBER: PCT/USO1/18340
PRIOR FILING DATE: 2001-66-05
PRIOR PILING DATE: 2001-06-10
PRIOR PILING DATE: 2001-06-12
PRIOR PILING DATE: 2001-06-13
PRIOR PELING DATE: 2001-06-13
PRIOR PELING DATE: 2001-06-13
PRIOR PELING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR PELING DATE: 2001-06-13
PRIOR PELING DATE: 2001-06-14
PRIOR PELING DATE: 2001-06-14
PRIOR PELING DATE: 2001-06-14
PRIOR PELING DATE: 2002-03-28
PRIOR PELING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR PELING DATE: 2002-03-28
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FILING DATE: 2001-06-06
APPLICATION NUMBER: PCT/US01/18340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: consensus sequence US-10-162-012-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                           Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : : | : | : | : | : | : | : | 135 GVKSINDWYAQRERGTAVGIENSSTVLGQAIA-PPALVIMQLAWGWRTMFVVIGLAGIVV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 PASLGRGRGAAAAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMV 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQLPSGILLDRLGPRIVLGAGLIFWSAMQALTGWV-NSFSHFILLRIGL-GIGEAPFMPA 134
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GENERAL INCRMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Gride-Saniago, Inmaculada
APPLICANT: Glu, Wei
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-190001
CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT PAPLICATION NUMBER: US 60/209,845
PRIOR FILING DATE: 2000-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 206.5; DB 4; Similarity 22.9%; Pred. No. 4.2e-10; D2; Conservative 82; Mismatches 200;
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                                                                                    Sequence 13997, Application US/09489039A
Patent No. 6610836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 102; Conservative
                                                          -09-489-039A-13997
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Best Local
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RESULT 10
US-09-252-991A-17560
i Sequence 17560, Application US/09252991A
i Sequence 17560, Application US/09252991A
i Patent No. 6551795
i GENERAL INFORMATION:
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO URRENT APPLICATION NUMBER: US 60/074,788
i PRIOR FILING DATE: 1999-02-18
i PRIOR FILING DATE: 1998-07-27
i NUMBER OF SEQ ID NOS: 33142
i SEQ ID NO 17560
i LENGTH: 506
## sequence 9335, Application US/09489039A

| Patent No. 6610836
| GENERAL INFORMATION:
| APPLICANT: Gary Breton et. al
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
| TITLE OF INVENTION: PNEUMONIARE FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REPERBNCE: 2709.2004001
| CURRENT APPLICATION NUMBER: US/09/489,039A
| CURRENT FILING DATE: 2000-01-27
| PRIOR APPLICATION NUMBER: US 60/117,747
| PRIOR APPLICATION NUMBER: US 60/117,747
| PRIOR FILING DATE: 1999-01-29
| NUMBER OF SEQ ID NOS: 14342
| SEQ ID NO 9335
| LARNOTHU: APPLICATION NUMBER: US 60/117,747
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BACKON et al.
TITLE OF INVENTION: BACKANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF EGG ID NOS: 8252
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Best Local Similarity 21.6%; Pred. No. 2.5e-09;
Matches 99; Conservative 71; Mismatches 174;
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US-09-328-352-5768
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RESULT 9 US-09-489-039A-9335

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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
                                            13
                                                                                     118 DRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIFF 177
                                                                                                              | : | : | : | : | : | OTAIIGFIASDLVQEWGVEKSALGPVMSAALVGLAVGALTAGPLADRIGRKKVLIMSIVV 109
                                                                                                                                                                      WSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNTRTLMLSVFYFA 237
                                                                                                                                                                                                                                                                                        LGDQLKARTSWLRDMKALIRNRSYVFSSLATSAV---SFATGA-----L 332
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                                                                                                                                                                                                                                                           238 IPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVP-----ATKRGHADQ 291
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                                                                                                                                                                                                   391 KTQRADP-LVCAVGMLGSAIFICLI-FVAAKSSIVGAYICIFVGETLLFSNWAITA-DIL
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                                               Gaps
                                            909
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6.4%; Score 186; DB 4; Length 463;
21.9%; Pred. No. 3.2e-08;
                                          68; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 TSWLPLLIRETGASMSQASIITALFPLGGGIGVLILGAL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10722, Application US/09489039A Patent No. 6610836
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TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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SEQ ID NO 10722
                                          Conservative
                    Similarity
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                                          82;
Query Match
Best Local S
Matches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 YITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVP-----ATKRGHADQLGDQLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 ARTSWLRDMKALI-------RINESYVFSSLATSAVSFATGALGMWIPL 338
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                                                                                                                                                                                                              4 RRRAGFIRAARRPAPASQ--SARRRVAARQARRGRRSQTRSTPAAQRNQVMPDAPAS---
                                                                                                                                                                    25 RRR----RGAORGAGGSGCCGARGAGGAGVSAAGDEVQTLSGSVRRAPTGPPGTPGC
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING 7
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING 7
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1099-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10827
LENGTH: 463
                                                                              Query Match 6.4%; Score 188; DB 4; Length 506; Best Local Similarity 20.1%; Pred. No. 2.4e-08; Matches 121; Conservative 72; Mismatches 218; Indels 192;
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Patent No. 6610836
GENERAL INFORMATION:
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               ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17560
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363 FGALGWPVISD-----TAPKEIVGLCGGVFNVFGNVASIVTPLVIGYL-
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ORGANISM: Klebsiella pneumoniae
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US-09-711-164-428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 SSLATSAVSFATGALGMWIPLYL--HRAQVVQKTABTCNSPP-CGAKDSLIFGALTCFTG 374
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                                                                                                                                                                    330 GRII-----SRIGKYRLFPILGTLLGVTGMV------LLIRITIHSPLWQ----- 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 ILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ARTSWLRDMKALIRNRSYVF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKSSIVGAYICIFVGET 434
                                                                       ------VCAVGMLGSAIFICLIFVAAKSSI---VGAYICIFVGETLLFSNWAIT 443
      AQVVQKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPL---- 398
                                                                                                                                        444 ADILMYVVIPTRRATAVALQSPTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGY 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I FIVTAVNYADRATLSIAGTEVAKELQLSAVSMGYIFSAFGWAYLLMQIPGGWLLDKFG 81
                                                                                                                                                                                                                                                                                                                 Sequence 258, Application US/09492709A

Sequence 258, Application US/09492709A

Sequence 258, Application US/09492709A

GENERAL INFORMATION

APPLICANT: Trewick, John

APPLICANT: Trewick, John

APPLICANT: Carr, Carn U.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: ESCHERICHIA COLI

FILE REPERENCE: ELITRA.001A

CURRENT APPLICANT: 2000-01-27

NUMBER OF SEQ ID NOS: 485

SOFTWARE: FELSER OF Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 SKKVYTYSLFFWSLFTFLQGFVDMFPLAWAGISMFFWRFWLGFSEAPSFPANARIVAAWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 TKNTRTLMLSVF----YFAIPLGSG-LGYITGSSVKQAAGDWHWALRVSPVLGMITGTLI
                                                                                            272 NRSFLLCSLIGFVIGMSLFGSVTFLPLYLQVVKEATPTEAGLQLIPLMGGLLLTS--IIS
                                    ------NDP-----QLWCILAF-GIVGIIGFIYEERMAAEPIIPLALFR
                                                                                                                                                                                                          558
                                                                                                                                                                                                                                   ---LYLFTGVLGAGIGIVMQVLVLAVQNAMPAQMYGVATSGVTLFRSIGGSIGVAL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                          504 ALMLCPFVVVLG-GMFFLATALFFVSDRARAEQHLGERRAGVRVVHQRGPGFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
6.2%; Score 182; DB 4; Length 444;
Best Local Similarity 21.2%; Pred. No. 6.9e-08;
Matches 98; Conservative 69; Mismatches 218; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 LILVPATKRGHADQLGDQLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: E. Coli
US-09-492-709A-258
                                                                                                                                                                                                                                                                                              RESULT 13
US-09-492-709A-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 258
LENGTH: 444
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Sequence 428, Application US/09711164
| Patent No. 6589738
| GENERAL INFORMATION: APPLICANT: POSSYTH, R. Allyn
| APPLICANT: Ohlsen, Kari
| APPLICANT: Zyskind, Judith
| TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERE
                                                                                                                                                                                             RESULT 14

US-09-489-039A-12384

Sequence 12384, Application US/09489039A

Facquence 12384, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

TITLE OF INVENTION: PRECONCEC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRESENCE: 2709-2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 CIFVGETLLFSNWAITADILMYVVIPTRRATAV-ALOSFTSHLLGDAGSPYLIGFISDLI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLILILVPATKR----GHADQLGDQLKAR-----TSWLRDMKALIRNRS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 GGLGILFTLVWWRFYHEPHESRTANDAELEYIGENSINNKIONVPFNW-RDARRLLGCRO 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 YVFSSLA----TSAVSFATGALGMWIPLYLHRAQVVQ--KTAETCNSPPCGAKDSLIFG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 NRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AITCFIGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKSSIVGAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRTLMLSVFYFAI PLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMI------T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.2%; Score 180; DB 4; Length 442; Best Local Similarity 22.2%; Pred. No. 1e-07; Matches 104; Conservative 72; Mismatches 190; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 RQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATALFFVSDRARAE 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534
                                                                                                       ---VSELHSFNAALVF----VGCSALMAMVCYLFVVGDIKRME
                                                         DSPLWEFLSLGYALMLCPFVVVLGGMFFLATALFFVSDRARAE
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20;
                                                                                                                                                                                                                                                                                                                                         110 LGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVPICSFMVAAPIFGYLGDRFNRKV 169
                                                                                                                                                                                                                                                                                                                                                                                                                 170 ILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNTRTL 229
                                                                                                                                                                                                                                                                                                                                                                      456 RATAVALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                         401 AVGMLGSAIFIC-LIFVAAK-SSIVGAYICIFVGETLLFSNWAITADI--LMYVVIPTR- 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 VVGLITSFIFLCPLFFISVKNSSLIG--LCLF---GLMFTNLGIAGLVPKFIYDYFPTKL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 MLSVFYFAIPLGSGLGYITGSSVKOAAGDWHWALRVSPVLGMITGTLILILVPATKRGHA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 DQLGDQLKARTSWLRDMKALIRNRSYVFSSLATSAVSF----ATGALGMWIPLYLHR--- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 AQVVQKTAETCNSPPCGAKDSLIFGAI--TCFTGFLGVVTGAGATRWCRLKTQRADPLVC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 RGLGTGL-IYNLGATGGMAAPVLATYISG------YYGLGVSL---FIVTVA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 NTVVISTLMTIAG-----KKKAF 304
                                                                                                                                                                                                                                                                    6.0%; Score 176.5; DB 4; Length 425;
22.7%; Pred. No. 2e-07;
tive 73; Mismatches 184; Indels 77; Gaps
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
FRIOR APPLICATION NUMBER: US 60/164415
FRIOR PILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 428
TYPE: DATE: 1299-11-9
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 22.7*
Matches 98; Conservative
                                                                                                                                                                                            TYPE: PRT GRGANISM: Escherichia coli US-09-711-164-428
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October 23, 2004, 12:53:58 ; Search time 88 Seconds (without alignments) 2082.357 Million cell updates/sec
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2920
1 MMCLECASAAAGGAEEEEAD......VHQRGPGFATALAHRVVGAS 566
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 48, Appl	Sequence 9, Appli	Sequence 5, Appli	Sequence 55, Appl	Sequence 50, Appl	Sequence 251, App	Sequence 52, Appl	Sequence 2641, Ap	Sequence 12, Appl	Sequence 126, App	Sequence 2, Appli	Sequence 23, Appl	Sequence 160, App
SUMMARIES	US-10-085-198-48	US-10-168-651-9	US-10-024-623-5	US-10-154-419-55	US-10-146-733-50	US-10-648-593-251	US-10-403-571-52	US-10-264-237-2641	US-10-168-651-12	US-10-169-395-126	US-09-860-232A-2	US-10-297-022-23	US-09-826-734-160
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% Query Match Length DB ID	2995	398	528	528	528	528	507	455	476	476	512	512	193
% Query Match	100.0	67.7	44.5	44.5	44.5	44.5	43.0	41.8	40.0	40.0	37.1	37.1	33.4
Score	2920	1978	1298	1298	1298	1298	1256.5	1222	1167	1167	1084	1084	916
Result No.	1	7	m	4	'n	φ	7	80	6	10	11	12	13

PALM.

14	855	29.3	531	14	10-154-41	81,	Appl
15	852	29.3	531	14	10-146-733-3	31,	Appl
16	779	26.7	299	10	39-809-391-3	396	App,
17	779	26.7	299	10	US-09-882-171-396	396	, App
18	779	26.7	299	14	10-164-861-	396	App,
19	672	23.0	424	2	US-09-809-391-555	555	, App
20	672	23.0	424	10	US-09-882-171-555	555	, App
21	672	23.0	424	14	US-10-164-861-555	555	App,
22	644	22.1	229	15	US-10-108-260A-3290	329	0, Ap
23	559	19.1	343	14	US-10-097-065-395	395	, App
24	559	19.1	343	14	US-10-372-876-395		
25	553	18.9	304	14	US-10-097-065-153		
56	553	18.9	304	14	US-10-372-876-153	Sequence 153,	App ,
27	534	18.3	106	10	US-09-826-734-246		
28	406	13.9	219	14	US-10-097-065-394		
29	406	13.9	219	14	US-10-372-876-394		
30	406	13.9	220	14	US-10-097-065-248		
31	406	13.9	220	14	US-10-372-876-248		
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33	396		136	2	US-09-809-391-554		
34	396		136	10	US-09-882-171-554		
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36	357.5		257	σ	US-09-860-232A-19	19,	Appl
37	276		118	15		28	2, Ap
38	268		412	15	US-10-425-114-49922	Sequence 49922,	22, A
39	252		453	14	US-10-369-493-23684		84, A
40	252		480	16	US-10-437-963-125320		320,
41	221		243	15	US-10-424-599-195951		951,
42	219		546		US-10-369-493-21873	Sequence 21873	73, A
43	218.5		549	<u>ο</u>	US-09-946-763-2	Sequence 2, Appli	ppli
44	218.5		549		US-09-738-626-3926		AD,
45	216.5	7.4	417	o	US-09-815-242-10592		2, A

## ALIGNMENTS

Sequence 48, Application US/100 GENERAL INFORMATION: GENERAL INFORMATION: APPLICAMY: ALSOBROOK et al., TITLE OF INVENTION: PLO2-279 CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2002-02- PRIOR PILING DATE: 2001-03-16 PRIOR PILING DATE: 2001-03-16 PRIOR PILING DATE: 2001-03-16 PRIOR PILING DATE: 2001-08-13 PRIOR PILING DATE: 2001-08-13 PRIOR PILING DATE: 2001-08-13 PRIOR PILING DATE: 2001-08-13 PRIOR PILING DATE: 2001-08-14 PRIOR PILING DATE: 2001-08-15 PRIOR PILING DATE: 2001-08-16 PRIOR PILING DATE: 2001-08-16 PRIOR PILING DATE: 2001-02-27 PRIOR PILING DATE: 2001-02-27 PRIOR PILING DATE: 2001-06-20	-10-085-198-48 Sequence 48, Application US/10085198 Sequence 48, Application US/10085198 GENERAL INFORMATION: APPLICANT: Alsobrook et al. APPLICANT: Alsobrook et al. APPLICANT: Alsobrook et al. APPLICANT: Alsobrook et al. APPLICANT: Alsobrook et al. APPLICANTON: Proteins and Nucleic Acids FILE REFERENCE: 21402-279 CURRENT APPLICATION NUMBER: US/10/085,198 CURRENT APPLICATION NUMBER: 60/274, 401 PRIOR APPLICATION NUMBER: 60/276, 401 PRIOR APPLICATION NUMBER: 60/216, 801 PRIOR PILING DATE: 2001-08-13 PRIOR APPLICATION NUMBER: 60/312, 840 PRIOR PILING DATE: 2001-08-16 PRIOR PILING DATE: 2001-03-20 PRIOR APPLICATION NUMBER: 60/271, 840 PRIOR PILING DATE: 2001-03-20 PRIOR APPLICATION NUMBER: 60/290, 695 PRIOR APPLICATION NUMBER: 60/290, 695 PRIOR PILING DATE: 2001-04-21 PRIOR APPLICATION NUMBER: 60/290, 695 PRIOR PILING DATE: 2001-04-21 PRIOR PILING DATE: 2001-04-20 PRIOR PILING DATE: 2001-04-20 PRIOR PILING DATE: 2001-04-20 PRIOR PILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: 60/272, 405 PRIOR PILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: 60/272, 405 PRIOR PILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: 60/272, 405 PRIOR PILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: 60/272, 405 PRIOR PILING DATE: 2001-02-28 PRIOR APPLICATION NUMBER: 60/272, 405 PRIOR PILING DATE: 2001-02-28 PRIOR PILING DATE: 2001-03-28	sic Acids	s Encoding e File Wra	ding Sam Wrapper	Ψ	ы. 0
; SEQ ID NO 48 ; LENGTH: 566 ; TYPE: PRT						

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                                                        Length 566;
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Sequence 9, Application US/10168651

Senemal INCYTE GENOMICS, INC.

APPLICANT: BAUGHN, Mariah R.

APPLICANT: BAUGHN, Mariah R.

APPLICANT: BAUGHN, Mariah R.

APPLICANT: BAUGHN, Manice

APPLICANT: AU-YOUNG, Janaice

APPLICANT: LU, Dyung Aina M.

APPLICANT: LAL, Preeti

APPLICANT: AZIMZAI, Yanga APPLICANT: AZIMZAI, Yalda

APPLICANT: AZIMZAI, Yalda

APPLICANT: AZIMZAI, Yalda

APPLICANT: YUE, Henry

APPLICANT: YAO, Monique G.

APPLICANT: YAO, Monique G.

APPLICANT: KHAN, Yarom

APPLICANT: HANO, YI TOM

APPLIC
                                                          DB 15;
                                                        Query Match 100.0%; Score 2920; DB 15; Best Local Similarity 100.0%; Pred. No. 8.4e-216; Matches 566; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGVRVVHQRGPGPGTALAHRVVGAS 566
; ORGANISM: Homo sapiens
US-10-085-198-48
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PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758; 60/181,625
    PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02
    NUMBER OF SEQ ID NOS: 54
    SOFTWARE: PERL Program
    SEQ ID NO 9
    LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10024623
; Sequence 5, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 8099, 46455, 54414, 53763, 67076, 67102, 44181,
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: NNI-214CP
CURRENT APPLICATION NUMBER: US 60/256,240
PRIOR PLICATION NUMBER: US 60/256,240
PRIOR PLING DATE: 2000-12-18
PRIOR PLLING DATE: 2000-12-18
PRIOR PLLING DATE: 2000-12-18
PRIOR PLLING DATE: 2000-12-18
PRIOR PLING DATE: 2000-12-18
PRIOR PLING DATE: 2000-12-18
SPIOR APPLICATION NUMBER: US 60/258,028
PRIOR PLING DATE: 2000-12-18
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Incyte ID No. US20030171275A1 3232992CD1
US-10-168-651-9
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67.7%; Score 1978; DB 14;
Best Local Similarity 99.0%; Pred. No. 1.3e-143;
Matches 384; Conservative 2; Mismatches 2;
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; ORGANISM: Homo sapiens
US-10-024-623-5
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:

APPLICANT: CULTIS, ROTY A.J.
APPLICANT: CULTIS, ROTY A.J.
APPLICANT: CULTIS, ROTY A.J.
APPLICANT: CULTIS, ROTY A.J.
APPLICANT: GLIGKEMBANN: MAILS A.
APPLICANT: GLIGKEMBANN: MAILS A.
APPLICANT: GLIGKEMBANN: MAIN STATEMBERS
TITLE OF INVENTION: NOVEL TWIK-5, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
TITLE OF INVENTION: AND USES THEREPOR.
TITLE OF INVENTION: AND USES THEREPOR.
TITLE OF INVENTION: AND USES THEREPOR.
TITLE OF INVENTION: AND USES THEREPOR.
THING DATE: 2000-02-9
PRIOR PELICATION NUMBER: US 60/185, 938
PRIOR PLING DATE: 2000-02-9
PRIOR PELICATION NUMBER: US 60/195, 734
PRIOR PLING DATE: 2000-04-30
PRIOR PELICATION NUMBER: US 60/195, 993
PRIOR PLING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/195, 993
PRIOR PLING DATE: 2000-04-26
PRIOR PLING DATE: 2000-09-19
PRIOR PELICATION NUMBER: US 60/235, 018
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-25
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                                             62 VAVLCYINLLNYMDRFTVAGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDR
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Sequence 55, Application US/20030143675A1

Sequence 55, Application No. US20030143675A1

Sublication No. US20030143675A1

Subblication No. US20030143675A1

Subblication No. US20030143675A1

Subblicant: Glucksman, Maria Alexandra

APPLICANT: Glucksman, Maria Alexandra

Subblicant: Glucksman, Maria Alexandra

Subblicant: Glucksman, Maria Alexandra

Subblicant: Glucksman, Maria Alexandra

Subblicant: Sofic Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie Sofie
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                                                                                                                                                                                                                                                                                     FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
                                                                                                                                                                                                                                                                                                                                                                                                                285 KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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; Pred. No. 3.1e-91;
62; Mismatches 162; Indels
                                                                   Indels
Query Match
44.5%; Score 1298; DB 13;
Best Local Similarity 53.4%; Pred. No. 3.1e-91;
Matches 275; Conservative 62; Mismatches 162;
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ilarity 53.4%;
Conservative 62
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; ORGANISM: Homo sapiens
US-10-154-419-55
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Matches 275; Conserva
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KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 PRGAVERHSDLPPLNPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLLRS 301
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; Sequence 52, Application US/10403571
; Publication No. US20040068763A1
; GENERAL INFORMATION:
; APPLICANT: Hopkins, Nancy
; APPLICANT: Golling, Gregory
; APPLICANT: Galling, Gregory
; APPLICANT: Sun, Zhoaxia
; TITLE OF INVENTION: Developmental Mutations in Zebrafish
; TITLE OF INVENTION: Developmental Mutations in Zebrafish
; FILE REFERENCE: 01997/539002
; CURRENT PILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/368,760
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 159
; SCOTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
LENGTH: 507
                                                                                                                                                                                                                                                                                                              53 AGDEVQTLSGSVRRAPTGP-PGTPGTPGCAATAKGPGAQQPKPASLGR-
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53.4%; Pred. No. 3.1e-91;
tive 62; Mismatches 162;
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                       US/10/648,593
FILE REFERENCE: D0273 NP
CURRENT APPLICATION WUMBER: US/10/648,5
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER: OF SEQ ID NOS: 557
SEQ ID NO 251
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.4%
Matches 275; Conservative
                                                                                                                                                                                   , ORGANISM: Homo sapiens
US-10-648-593-251
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US-10-403-571-52
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Publication No. US20040106132A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENITON: IDENTIFICANTINON OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
TITLE OF INVENITON: INTERACT WITH ANDOR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENITON:
PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRGHADQLGDQLKAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
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44.5%; Score 1298; DB 14;
Best Local Similarity 53.4%; Pred. No. 3.1e-91;
Matches 275; Conservative 62; Mismatches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 ALFFVSDRARAEQHLGE--RRAGVR----VVHQRG
         PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/828,035
PRIOR FILING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-01
PRIOR PLING DATE: 2001-04-11
PRIOR PLING DATE: 2001-04-11
PRIOR PLING DATE: 2001-04-25
PRIOR PLING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 50
LENGTH: 528
                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-10-146-733-50
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CURRENT APPLICATION NUMBER: US/10/168,651

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758
60/181,625

PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02;
    61 FWSLVTLGSSPIPGEHFWLLLLTRGLVGVGEASYSTIAPTLIADLFVADQRSRMLSIFYF 120
                                                                415 FVAAKSSIVGAYICIFVGETILLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAG 474
                                                                                                                                                                                                                                                                                                                                                                                         361 SPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGTAIFIEADRRRAQ 420
                                                                                                                      297 KAR-TSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETC-N 354
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                                                                                                                                             SPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMPFLATALPFVSDRARAE
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OTHER INFORMATION: Incyte ID No. US20030171275A1 70064803CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS FILE REFERENCE: PI-0005 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 QHLGE--RRAGVR----VVHQRG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 LHVQGLLHEAGSTDDRIVVPORG 443
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Publication No. US20030171275A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INCYTE GENOMICS, INC
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NGUYEN, Danniel B.
YAO, Monique G.
GANDHI, Ameeni R.
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BURFORD, Neil
AU-YOUNG, Janice
LU, Dyung Aina M.
YANG, Junming
REDDY, Roopa
LAL, Preeti
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KHAN, Farrah A.
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NUMBER OF SEQ ID NOS: 54
SOFTWARE: PERL Program
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                  GAIEAHPEHTLHRISWLADMKALCRNPGFILSTFGFTAVAFVTGSLALWAPAFLFRAGVF 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILLVPATKR 286
                                                                                                                                                                                                                                                                                                                                                                                                       GHADQLGDQLKARTSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 QKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLG 406
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                                                                                 Length 507;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                             Query Match
43.0%; Score 1256.5; DB 15; Lengt
Best Local Similarity 56.4%; Pred. No. 4.6e-88;
Matches 251; Conservative 66; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR PELING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 VSDRARAEQHLGERRAGVRVVHQRG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2641, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
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US-10-264-237-2641
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-403-571-52
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NTRILMLSVFYPAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPAT 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 MLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQ 463
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                                                                                                                     FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK
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                                                 AAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDR
                                                                                                                                                                                                                                                                                                                                                                                                          344 QVVQKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVG
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Federn No. US20020028494A1
GENERAL INFORMATION:
FAPLICAPT CURTIS, Rory A.J.
TITLE OF INVENTION: 57256 AND 58289, NOVEL HUMAN
TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
FILE REPERENCE: 381552001500
CURRENT APPLICATION NUMBER: US/09/860,232A
CURRENT FILING DATE: 2001-05-17
FRIOR FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.1%; Score 1084; DB 9; Best Local Similarity 47.5%; Pred. No. 8.3e-75; Matches 223; Conservative 75; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                         LFFVSDRARAEQHLGE--RRAGVR----VVHQRG 551
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
IENGTH: 512
TYPE: PRT
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US-09-860-232A-2
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Publication No. US20040034192A1

GENERAL INFORMATION:

APPLICANT: KATO, Seish

APPLICANT: KATO, Seish

APPLICANT: KATO, Seish

TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOWAINS AND DNAS ENCODING

TITLE OF INVENTION: HUMAN PROTEINS

FILE OF INVENTION: HUMAN PROTEINS

FRICH REPERBACE: 2000-01-02

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-01

FRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463
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                                                                                                                                                                                                                                                                                                                                                                            242 PRGAVERHSDLPPLNPTSWMADLRALARN------270
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                                                 105 AAILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFWVAAPIFGYLGDR 164
                                                                                                                                              FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
                                                                                                                                                                         NTRTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPAT 284
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    61
                                                                          AGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEEPEVPDQEGLQRITGLSPGRSALI
2 AGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEEPEVPDQEGLQRITGLSPGRSALI
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llarity 49.4%; Pred. No. 3.2e-81;
Conservative 53; Mismatches 141;
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US-10-169-395-126
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Best Local Simil
Matches 254; C
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Sequence 160, Application US/09826734
Publication No. US20030017457A1
GENERAL INFORMATION:
APPLICANT: Fernandes, Elna R.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Wartin D.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Ramesha
TITLE REFERENCE: 15966-754
CURRENT APPLICANTION NOVEL POLYMUCLEOLIDES and Polypeptides Encoded Thereby
FILE REFERENCE: 15966-754
CURRENT PILING DATE: 2001-04-05
FRIOR PEPLICATION NUMBER: 60/195,576
FRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 270
SOFTWARE FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAKES FREAK
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                                                                                                                                                                                                                                                                                                                                                           189 PQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNTRTLMLSVFYFAIPLGSGLGYIT 248
                                                                                                                                                                                                                                                                                                                                                                                          GSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKRGHADQLGDQLKA--RTSWLRDM 306
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                                                                                                                                                                         ||:| || :||: || ||:||: || GALTIMTGVIGVILGAEASRRYKKVIPGAEPLICASSLLATAPCLYLALVLAPTTLLASY
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                                                                                                                                                                                                                                               129 IQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIFFWSAVTFSSSFI
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                                 Length 512;
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                            ; Score 1084; DB 14; Length
; Pred. No. 8.3e-75;
75; Mismatches 163; Indels
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                                 37.1%;
                                                                                    223; Conservative
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Matches 190; Conservative
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ORGANISM: homo sapiens
                                                           Similarity
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                               Query Match
Best Local S
Matches 223
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CURRENT APPLICATION NUMBER: US/10/297,022
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/208,424, 60/209,001; 60/210,588; 60/212,335; 60/213,747;
PRIOR FILING DATE: 2000-05-26; 2000-06-01; 2000-06-08; 2000-06-16; 2000-06-22; 2000-06-08 SOCID NOS: 54
SOFTWARE: PERL Program
                                                                                    367 GAITCFIGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKSSIVGAY 426
                                                                                                                                                                                                                                                                      427 ICIFVGETLLFSNWAITADILMYVVIPTRRATAVALOSFTSHLLGDAGSPYLIGFISDLI 486
                                                                                                                                                                                                                                                                                                        GSAVTMLTGNWRWALRVMPCLEAVALILLILLVPDPPRGAABTQGEGAVGGFRSSWCEDV 251
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                                                     307 KALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETCNSPPCGAKDSLIF
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030216310A1 1713377CD1
US-10-297-022-23
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PPLICANT: HILLMAN, Jennifer L.
ITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/10297022 Publication No. US20030216310A1 GENERAL INFORMATION:
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GANDHI, Ameena R.
TRIBOULEY, Catherine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEARNEY, Liam
ELLIOTT, Vicky S.
SEILHAMER, Jeffrey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Christopher M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLICKY, Jennifer L.
BOROWSKY, Mark L.
BURFORD, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SANJANWALA, Madhu S.
RAUMANN, Brigitte E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAO, Monique G.
RAMKUMAR, Jayalaxmi
AU-YOUNG, Janice
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WALIA, Narinder K.
YUE, Henry
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BAUGHN, Mariah R.
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ORGANISM: Homo sapiens
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40.0%; Pred. No. 3.4e-57;
ative 82; Mismatches 173; Indels
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; ORGANISM: Homo sapiens
US-10-146-733-31
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                         490 KDKAR 494
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SEQ ID NO 31
LENGTH: 531
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                                                                       71 PPGTPGTP-----GCAATAKGPGAQQPKPASLGRGRGAAAILSLGNVLNYLDRYŢ 121
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Best Local Similarity 40.0%; Pred. No. 3.4e-57;
Matches 194; Conservative 82; Mismatches 173;
                                                                                                                                                                           SAVSFATGALGMW 335
                                                                                                                                                                                                                         181 SAVSFATGALGMW 193
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                                                                                        242 SGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILLLVPATKRGHADQLGDQLKA--- 298
                                                                                                     299 RTSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTABTCNSPPC 358
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283416 segs, 96216763 residues

Searched:

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PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	3 3 3 4 4 8	35 37	8 6 4 8 0 0	4 4 4 1 2 4	44

## **ALIGNMENTS**

RESULT 1 T19232 hypothetical protein C13C4.5 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C.Accession: T19232 R.Harris, B.	submitted to the EMBL Data Library, March 1997 A;Reference number: 219095 A;Recession: T19295 A;Stcatus: preliminary; translated from GB/EMBL/DDBJ A;Wolecule type: DNA A;Residues: 1-531 <wil> A;Residues: 1-531 <wil> A;Cross-references: UNIRROT:001927; EMBL:292825; PIDN:CAB07311.1; GSPDB:GN00023</wil></wil>	A;Experimental Bource: clone C13C4 C;Genetics: AjGene: CESP:C13C4.5 A;Map position: 5 A;Introns: 78/1; 145/3; 269/2; 341/3; 389/3; 411/3; 500/1	Query Match 29.3%; Score 855; DB 2; Length 531; Best Local Similarity 40.0%; Pred. No. 1.5e-50; Matches 194; Conservative 82; Mismatches 173; Indels 36; Gaps 9;	Qy 71 PPGTPGTPGCAATAKGPGAQQPKPASLGRGRGAAAAILSLGNVLAYYLDRYT 121	QY 122 VAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIFFWSAV 181		QY 242 SGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKRGHADQLGDQLKA 298	QY 299 RISWLRDMKALIRNRSYVFSSLATSAVSFATGALGMMIPLYLHRAQVVQKTABTCNSPPC 358     :	OY 359 GAKDSLIFGAITCFTGFLGVVTGA-GATRWCRLKTQRADPLVCAVGMLGSAIF 410	OY 411 ICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALGSFTS 467
RESULT T19232 hypothe C,Speci C,Date: C,Acces R,Harri	submitt A,Refer A,Acces A,Statu A,Molec A,Cose	A;Exper C;Genet A;Gene: A;Map p	Query Best Match	ò q	රු යි	oy G	. අ	ço Go	S da	ço a

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A;Molecule type: DNA
A;Residues: 1-411 <WIL>
A;Cross-references: UNIPROT:Q19235; EMBL:Z69788; PIDN:CAA93644.1; GSPDB:GN00028; CESP:FC
A;Experimental source: clone F09A5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2g22730 [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (Mouse-ear cress)
C.Species: Arabidopsis thaliana (Mouse-ear cress)
C.Species: Oz-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C.SACCession: B84616
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., Rature 402, Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of Chronosome 2 of the plant Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.3%; Score 681; DB 2; Length 411; Best Local Similarity 36.7%; Pred. No. 7e-39; Matches 149; Conservative 79; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411
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submitted to the EMBL Data Library, February 1996 A;Reference number: 219301 A;Accession: T20623 A;Status: preliminary; translated from GB/EMBL/DDBJ
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A, Residues: 1-507 <STO>
A, Cross-references: UNII
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A, Map position: 2
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C;Species: Caenorhabditis elegans
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C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19854
A;Sims, M.

Bubmitted to the EMBL Data Library, March 1996
A;Reference number: Z19187
A;Accession: T19854
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A;Accession: Caenorics: UNIPROT:Q18545; EMBL:Z70307; PIDN:CAA94337.1; GSPDB:GN00022; CESP:C3
A;Experimental source: clone C39E9
A;Generics:
A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Accession:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                    112 NVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVIL 171
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20623
R;Gajadsty, S.
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Best Local Similarity 38.8%; Pred. No. 6.9e-48;
Matches 173; Conservative 82; Mismatches 167; Indels
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QY         295 QLKARTSWLRDMKALIRNRSYVESSLATSAVSFATGALGWWIPLYLH 341           Db         506 QIKTKTPKSKNLVVLFGKDLKALFSEKVFIVNVLGYITYNFVLGAYSYWGPKAGFGIY 563           QY         342 RAQVVQKTABTCNSPPCGAKDSLIFGAITCFTGFLGVYTGAGATRWCRLKTQRADDLVCA 401           Db         564KMKNADMIFGGLTICGIIGTLGGSYVLDRINATLSNTFKLLAA 607           QY         402 VGMLGSAIFICLIFVAAKSSIVGAYICIF-VGETLLFSNWAITADILMYVVIPTRRATAV 460           Db         608 STLLGAAFCFTAFLMKNWYAFIALFAVGEILIFAPQAPVNFVCHCVPRNLRPLSM 663           QY         461 ALQSFTSHLLGDDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFL 520           Db         664 ASSTVLIHILGDVPSSPLYGKMQDHLKNWRKST	RESULT 6 GG7290 major facilitator family transporter CC0336 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: G87201 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: G87201 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 R;Mierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelb, B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H. n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Frase Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001 A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-438 <sto- 112;="" 12="" 147="" 14;="" 220;="" 25.3%;="" 38;="" 5.2e-12;="" 70<="" 73;="" 93="" a;cross-references:="" a;gene="" best="" cc0336="" conservative="" cuery="" db="" g;genetics:="" gaps="" gb:ae005673;="" indels="" kaetagrggryryvvlamlilaytfnfldr-qilgilagsikaelhltdtqlglmggvaf="" kpaslgrgrgaaaailslgnvlnyldrytvagvll-diqqhfgvkdrgagllqsv-p="" local="" match="" matches="" mismatches="" nid:g13421483;="" no.="" pidn:aak22323.1;="" pred.="" query="" qy="" similarity="" th="" uniprot:q9ab95;=""><th>QY 148 ICSFMVAAPIFGYLGDRFNRKVILSCGIFFWSAVTFSSSFIPQQYFMILVLSRGLVGIGE 207                                       </th><th>268 VLGMITGTLILLIUVPATKRGHADQL-GDQLKARTSWLRDMKALIRNRSYVFSSLAT :  </th><th></th><th>OY 441 AITADILMYVVIPTRRATAVALQSFTSHLIGDAGSPYLIGFISDLIRQSTKDSPLWEFLS 500  1                                    </th></sto->	QY 148 ICSFMVAAPIFGYLGDRFNRKVILSCGIFFWSAVTFSSSFIPQQYFMILVLSRGLVGIGE 207	268 VLGMITGTLILLIUVPATKRGHADQL-GDQLKARTSWLRDMKALIRNRSYVFSSLAT :		OY 441 AITADILMYVVIPTRRATAVALQSFTSHLIGDAGSPYLIGFISDLIRQSTKDSPLWEFLS 500  1
Db 10 PPVTETTSRCYSTSSSTPLAELETVRSLEIVESSSSLSPVWLLVIFCIINLLNYMDRGAI 69  123 AGVLLDIQQHFGVKDRGAGLLQSVFICSFWVAAPIFGYLGDRF 165	Qy   369   ITCFTGFLGVVTGAGATRWCRLKTQRADDLVCAVGMLGSAIFICLIFVAAKSSIVGAYIC   28	PESULT 5 T05899 T05899 T05899 T05899 T05899 T05899 T05899 T05899 C; Date: 09-bpr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004 C; Date: 09-bpr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004 C; Date: 09-bpr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004 C; Date: 09-bpr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004 R; Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewe submitted to the Protein Sequence Database, April 1998 A; Reference number: 215456 A; Rocession: T05899 A; Molecule type: DNA A; Residues: 1-746 < BEV> A; Cross-references: UNIRROT:049546; EMBL:AL021684 A; Cross-references: Cultivar Columbia; BAC clone F6H11	A.Map position: 5 A;Map position: 5 A;Introns: 54/2; 99/2; 134/2; 198/3; 235/3; 265/2; 309/2; 360/2; 395/2; 420/3; 445/3; 48 A;Note: F6H11.180 Query Match Best Local Similarity 24.5%; Pred. No. 1.8e-16; Matches 119; Conservative 72; Mismatches 185; Indels 109; Gaps 15;	107 ILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGILQSVFIC	150 SFWNAAPIGGYLGDRENRKVILSCGIFFWSAVIFSSSFIPQQY  121	Qy 253 KQAAGDWHWALRVSPVLGMITGTLILIUVPATK-RGHADQLGD 294

GSPDB

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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Recession: E87557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-519 <STO>
A;Cross-references: UNIPROT:Q9A5G4; GB:AE005673; NID:g13424039; PIDN:AAK24457.1; GSPDB:CCGenetics:
A;Genetics:
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A;Cross-references: UNIPROT: P39398; GB:AE000506; GB:U00096; NID:g2367377; PIDN:AAC77312
A;Experimental source: strain K-12, substrain MG1655
B;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
A) Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92
A;Reference number: S56314; MUID:95334362; PMID:7610040
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EFKELMAVTKILFGKMPVLHMVLGVTIASFGAYGSGAFVPSYFVRAFDLGL------ 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AAGDWHWALRVSPVLGMITGTLILILVPATKRGHA-------DQLGDQLKARTSWLR 304
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A;Molecule type: DNA
A;Residues: 262-453 <BUR>
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9.5%; Score 276; DB 2; Length 519;
Best Local Similarity 24.3%; Pred. No. 2.5e-11;
Matches 111; Conservative 71; Mismatches 188; Indels
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Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Recession: F83164
A;Retsidues: preliminary
A;Residues: 1-457 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9HVD8; GB:AE004879; GB:AE004091; NID:g9950901; PIDN:AAG0804
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4654
                                                                                                                                                                                                                             probable MFS transporter PA4654 [imported] - Paeudomonas aeruginosa (strain PAOI)
C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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                                                                                                : ||: | |: ||: 407 MRYAIYYGLSFYVVAAVLLILAS 429
                                                                   522
                                                                     LGYALML-CPFVVVLGGMFFLAT
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A,Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97253.1; PID:g537198
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C;Superfamily: hexuronate transporter
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Best Local Similarity 24.3%; Pred. No. 9.3e-10;
Matches 115; Conservative 79; Mismatches 212; Indels 68; Gaps
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8.6%; Score 252; DB 1; Length 453;
Best Local Similarity 24.3%; Pred. No. 9.3e-10;
Matches 115; Conservative 79; Mismatches 212; Indels
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hypothetical protein yjiz [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Species: Escherichia coli coli elementari che seboratichia coli dell'obseria dell'obseria n.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe Iller, L.; Grotheck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
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A;Molecule type: DNA
A;Residues: 1-453 <STO>
A;Cross-references: UNIPROT:Q8XEG8; GB:AE005174; NID:g12519379; PIDN:AAG59539.1; GSPDB:
A;Experimental source: strain O157:H7, substrain EDL933
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                                                                   128 -HSFTQFVLVRIGMGIGEAPMNPCGVKVINDWFNIKERGRPMGFFNAASTIGVAVSPPIL 186
                                                                                                                                              301
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A;Accession: S48313
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A;Residues: 1-546 <CHU
A;Residues: 1-546 <CHU
A;Crose-references: UNIPROT:P43581; EMBL:Z46255; NID:g559925; PIDN:CAA86344.1; PID:g5595
R;Aurakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanumitted to the EMBL Data Library, May 1995
B;Apscription: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces c. A;Reference number: S56186
A;Accession: S56243
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A;Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09227.1; PID:g836743; MIPS:YFL011
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submitted to the EMBL Data Library, April 1994

A;Reference number: 862302

A;Accession: 862302

A;Molecule type: DNA

A;Residues: 1-546 <MUW>
A;Cross-references: EMBL:D31600; NID:g836814; PIDN:BAA06493.1; PID:g893435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%; Score 219; DB 2; Length 546; 21.7%; Pred. No. 2e-07; tive 84; Mismatches 178; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fil0-117/Domain: transmembrane #status predicted <TM2>
Fil30-146/Domain: transmembrane #status predicted <TM3>
Fil55-171/Domain: transmembrane #status predicted <TM3>
Fil52-174/Domain: transmembrane #status predicted <TM4>
Fil324-240/Domain: transmembrane #status predicted <TM5>
Fil348-364/Domain: transmembrane #status predicted <TM5>
Fil372-428/Domain: transmembrane #status predicted <TM7>
Fil12-428/Domain: transmembrane #status predicted <TM7>
Fil41-497/Domain: transmembrane #status predicted <TM9>
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C;Superfamily: maltose transport protein MAL61
C;Keywords: sugar transport; transmembrane protein
F;48-64/Domain: transmembrane #status predicted <TW
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A,Cross-references: SGD:S0001883, MIPS:YFL011w
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Best Local Similarity 21.7%
Matches 108; Conservative
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A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Recession: D87557

A;Residues: Draliminary

A;Residues: 1-444 <STO>
A;Residues: 1-444 <STO>
A;Residues: 1-674 <STO>
A;Resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                major facilitator family transporter CC2485 [imported] - Caulobacter crescentus
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                                                                                                                                      348 IVPQATTSMMAVLLIGMALFCIHFAGT----SCWG-----LIHVAVASRMTASVGSIQNFA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKSTGLMAAIPFLFGAAGMLVNGYVTDWLVKGGMAPIKSRK----ICIIAGMFCSAAFTL 347
                                                                      LIFVAAKSS----IVG-AYICIFVGETLLFSNWAITADILMYVVIPTRRATAV-ALQSFT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 GIGEASYSTIAPTIIGDLFTKNTRTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWAL 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Caulobacter crescentus
Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hexose transport protein HXT10 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein F008; protein YFL011w
C;Species: Saccharomyces cerevisiae
C;Species: O2-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48313; S56243; S52302
R;Churcher, C.
submitted to the EMBL Data Library, September 1994
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                                                                                                                                                                                                         SHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFL 520
                                                                                                                                                                                                                                                | : : | | | | | : : SFICA-SFAPIITGFIVDTH-----SFRIALIICGCVTAAGALAYI 440
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Nature 390, 249-256, 1997
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Nature 390, 249-256, 1997
A, Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galls
A, Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuse, S.; Hosono, S.; Hullo, M.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinol, M.;
A, Authors: Lauber, J.; Lazarevic, V.; Tee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue,
Y.; M.; Ogawa, K.; Ogiwara, A.; Oddega, B.; Park, S.H.; Parro, V.; Poll, T.M.; Portectell
Rieger, M.; Rivolta, C.; Rocha, B.; Park, S.H.; Parro, V.; Poll, T.M.; Portectell
Rieger, M.; Rivolta, C.; Rocha, B.; Park, S.H.; Sadaie, Y.; Saco, T.; Scanlo,
A, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser,
A, Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyam
T.; Winters, P.; Wipat, A.; Tamanoto, H.; Yasumacto, K.; Yata, K.; Yoshida,
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Accession: A6983
A; Accession: A6983
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A; Residues: 1-422 <KUN>
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C; Construential source: strain 1
         Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ARKGVLFSRKVVLVTCLFSSAVLIGPAGLVATTAGAVTLVALSVFFLYLTGALYMAVIQD 343
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C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Cacesion: F87474
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 41354141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Status: preliminary
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PRVRATASAILFFLTSLIGLGPLAVGVASDLLRASLGPVQSLNLACAGASITWVASVV 455
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Aah65235 homo sapi
Qerg7 mus musculu
Qerg7 mus musculu
Qerub7 brachydanio
Q72113 brachydanio
Q931n7 mus musculu
Q86vu7 homo sapien
Q94212 mus musculu
Q71rb5 homo sapien
Q67rc55 homo sapien
Q67rc55 homo sapien
Q67rc55 homo sapien
Q67rc56 homo sapien
Q67rc56 homo sapien
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mus musculu
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                                                                                          October 23, 2004, 11:01:18 ; Search time 111 Seconds (without alignments) 2933.892 Million cell updates/sec
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                                                                                                                                                                                           1 MMCLECASAAAGGAEEEEAD......VHQRGPGPGTALAHRVVGAS 566
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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AAH65235
CAM6573
O9EQK0
O9UWB7
O9EUV7
O9EVV7
O9EVV7
OPECSS
OFEWD2
O7IRB5
AAQ15559
OFEWD2
OFEWD2
OFEWD2
OPEWD2
O9GQQ0
O9GQQQ
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Q9H2V7
Q7L541
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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2920
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Match Length DB
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	Q9gqp9 drosophila	Q8r119 mus musculu	Q9zq41 arabidopsis		Aas47627 arabidops	Aat41792 arabidops	Q9flg8 arabidopsis	049546 arabidopsis	Q6j2d6 pseudomonas	Q88bw0 pseudomonas	Aat35185 pseudomon	Q87xs1 pseudomonas	Q89ki2 bradyrhizob
QBMLDO	09GQP9	Q8R119	Q9ZQ41	QENMING	AAS47627	AAT41792	Q9FLG8	049546	Q6J2D6	Q88BW0	AAT35185	Q87XS1	Q89KI2
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## ALIGNMENTS

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11 MMCLECASAAAGGAEEEEBDAERRRRRGAQRGAGGSGCCGARGAGGAGVSAAGDEVQTL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNTRTLMLSVFYFAIPL 240
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                    QBIVWB;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to spinster-like protein (Fragment).
Homo sapinster-like protein (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.6%; Score 2761; DB 2; Best Local Similarity 99.3%; Pred. No. 7.1e-161; Matches 535; Conservative 2; Mismatches 2;
    619 AA
PRT;
  PRELIMINARY;
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90.88;
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SEQUENCE FROM N.A.

STRAIN-129; TISSUE-Mammary tumor. Brcal-/fl;

MEDLINE-238825; PubMed-1247932;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R.,

A Hopking R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toonhyuki S., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Waden P.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakebley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                    SWLRDWKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETCNSPPCGA 430
                                                                                                                                                      SIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAGSPYLIG 550
                                                                    KDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKS 420
                                                                                     KDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAKS 490
                                                                                                                                    SIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAGSPYLIG 480
 SWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETCNSPPCGA 360
                                                                                                                                                                                                                                    609
                                                                                                                                                                                                     FISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATALFFVSDRARAEQHLGE 539
                                                                                                                                                                                                                        Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; BC011467; AAH11467.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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STRAIN-129; TISSUE-Mammary tumor. Brcal-/fl;
Strausborg R.;
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GO; GO:001621; C:integral to membrane; IEX
GO; GO:0005215; F:transporter activity; IEX
GO; GO:0006810; F:transport; IEA.
InterPro; IPR005881; Sub_transporter.
Ffam; PP00083; Sugar tr; 1.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                       Created)
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01-DEC-2001 (TrEMBLrel. 19, Lo
01-MAR-2004 (TrEMBLrel. 26, Le
BC011467 procein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
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NON TER
SEQUENCE 590
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360
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                                                                                                                                                                                          TVAGVLLDIQQHFGVKDRGAGLLQSVFICSFMVAAPIFGYLGDRFNRKVILSCGIFFWSA
                                                                                                          SWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETCNSPPCGA
                                                                                    1 MMCLECASAAAGGAEEEEADAERRRRRRGAQRGAGGSGCCGARGAGGAGVSAAGDEVQTL
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TISSUB=Brain, and Pancreas;
MEDLINE=22386257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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MEDLINE=21238517; PubMed=11340170;
Nakano Y., Fujitani K., Kuthara J., Ragan J., Usui-Aoki K.,
Shimoda L., Lukacsovich T., Suzuki K., Sezaki M., Sano Y., Ueda R.,
Awano W., Kaneda M., Umeda M., Yamamoto D.;
"Mutations in the novel membrane protein spinster interfere with
programmed cell death and cause neural degeneration in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Score 2652; DB 2; Length 590;
Pred. No. 3.2e-154;
9; Mismatches 16; Indels
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Last annotation update)
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Mol. Cell. Biol. 21:3775-3788(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, C)
01-MAR-2001 (TrEMBLrel. 16, L6
01-07-2004 (TrEMBLrel. 28, L8
Spinster (SPINL protein).
                      Best Local Similarity 95.4%;
Matches 514; Conservative
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53 AGDEVQTLSGSVRRAPTGP-PGTPGCAATAKGPGAQQPKPASLGR-----GRGA-A 104
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302 RVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEISRRLRHSNPRADPLVCAT 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 QVVQKTABTC-NSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAV 402
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Schwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VAVLCYINLLNYMDRFTVAGVLPDIEQPFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AF212371; AA403301; --
EMBL; BCO08325; AA408355.1; --
EMBL; BCO08325; AA4189561.1; --
EMBL; BCO083261; AA4189561.1; --
EMBL; BCO08021; Cintegral to membrane; IEA.
GO; GO:0016021; Fitransporter activity; IEA.
GO; GO:0006210; Pitransport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 AA; 56629 MW; F1B9D2EB3F9F1B48 CRC64;
                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Interproj IPRO1818; Sub transporter.
Pfam: PF00083; Sugar tr; 1.
PROSITE; PS50850; MFS; 1.
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Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pancreas;
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RC TISSUE=Brain,

MEDLINE=2238257; PubMed=12477932;

MEDLINE=2238257; PubMed=12477932;

MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschank B. F., Tordan H., Moore T., Max S.I., Wang J., Haiber F.,

Brownstein M.S., Gares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.S., Ugdil T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ugdil T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lux Y., Gibbs R.A.,

RA Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ral Residy R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schuutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
422 QIVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VAGVLLDIQQHFGVKDRGAGLLQSVFICSFWVAAPIFGYLGDRFNRKVILSCGIFFWSAV 181
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-- EMBL; BC061156; AAH06156.1; --
InterPro; IPR007114; MFS.
InterPro; IPR05828; Sub_transporter.
PFam; PF00083; Sugar_tr;
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.4%; Score 1297; DB 2; 54.8%; Pred. No. 2.2e-71;
                                                          |:| :|| || || || 482 AIFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRG
                                      ALFFVSDRARAEQHLGE--RRAGVR----VVHQRG
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEQUENCE
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Q7L541;
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Best Local Similarity 53.4%
Matches 275; Conservative
Pfam; PF00083; Sugar Lr_j: PROSITE; PS50850; MF\overline{S}; 1. Transmembrane.
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                                         528 AA;
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AAH65235;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soarsa M.B., Bonaldow M.F., Carannor P.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., McWaman D.J., McKernan K.J., Marke J.J., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                        375 GSIVATYIFIFIGETLLSMWWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGDAGSPYLI 434
                                                                                                                                                                                                                                            GFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATALFFVSDRARAEQHLGE 539
                           SCLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKRGHADQLGDQLKAR-T 300
                                                                                SWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVVQKTAETC-NSPPCG 359
                                                                                              AKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFVAAK 419
                                                                                                                                                             SSDSLIFGLITCLTGVLGVGLGVEISRRLRHSNPRADPLVCATGLLGSAPFLFLSLACAR 374
                                                                                                                                                                                       SSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFTSHLLGDAGSPYLI 479
                                                                                                                                                                                                                                                          TLGSSFIPGEHFWLLLLTRGLVGVGEASYSTIAPTLIADLFVADQRSRMLSIFYFAIPVG 194
                                        Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                           528 AA
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Interpro, IPR007114; MFS.
Interpro, IPR005828; Sub_transporter.
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                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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05-JUL-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPINL protein.
Name=SPINL;
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05-JUL-2004
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                                                                                                                      16; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                         DB 2; Length 528;
                                                                                                                      Indels
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Last annotation update)
                                                   44.4%; Score 1297; DB 2; 53.4%; Pred. No. 2.2e-71; ive 62; Mismatches 162;
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BC03B6BF2BCB03A6
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56655 MW;
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                             2 AGSDTAPFLSQADDPDDGPVPGTPGLPGSTGNPKSEEPEVPDQEGLQRITGLSPGRSALI
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                             DB 2; Length 528;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                 Straubberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062335; AAH65235.1; -.
SEQUENCE 528 AA; 56655 MW; BC03B6BF2BCB03A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                          Query Match 44.4%; Score 1297; DB 2; 1
Best Local Similarity 53.4%; Pred. No. 2.2e-71;
Matches 275; Conservative 62; Mismatches 162;
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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Name=2210013K02Rik;
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                         TISSUE=Skin
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SEQUENCE FROM N.A.

STRAIN-FVB/N; TISSUG-Kidney;

MEDLINE-2238825; PubMed=1247932;

MEDLINE-2238825; PubMed=1247932;

MEDLINE-2238825; PubMed=1247932;

MAISCHUI S.P., Zeeberg B., Buerow K.H., Schamen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

MAISCHUL S.P., Zeeberg B., Bonaldo M.F., Gaavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

M. Rodriguez A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Minting M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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La Strausberg R.;
Lo the EMBL/GenBank/DDBJ databases
Lu Submitted (AFR-2002) to the EMBL/GenBank/DDBJ databases
Lu Submitted (AFR-2002) to the EMBL/GenBank/DDBJ databases
Lu Submitted LOCATION: Integral membrane protein (By similarity).

EMBL; BC026854; AAH26854.1;
RMGD; MGI.1920908; 2210013KO2Rik.
RMGD; MGI.1920908; 2210013KO2Rik.
RMGD; GO:0016021; C:integral to membrane; IEA.
RO; GO:0016515; F:transporter activity; IEA.
RMGD; GO:0005515; F:transporter activity; IEA.
RMGD; GO:000566; Lipocln_cytPABP.
RMCD: IPR00956; Lipocln_cytPABP.
RMCD: IPR00958; Sub_transporter.
Pfam; PF00081; Sugar_tr; 1.
RMCOMN_1: PROSITE; PS00213; LiPOCALIN; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 528 AA; 56708 MW; DDAB448D7D2B9E17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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522

us-10-085-198-48.rup

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107 ILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGILQSVFICSFMVAAPIFGYLGDRFN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 RKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHADQLGDQLKARTSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVV 346
                   QVVQKTAETC-NSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAV 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Zebrafish yolk-specific not really started (nrs) gene is a vertebrate homolog of the Drosophila spinster gene and is essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KTNMLSIFYFAI PVGSGMGYIVGSKVDTVAKDWHWALRVTPGLGLLAVFLLMLVVQEPKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 RILMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKR
                                                     GMLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVAL
                                                                                                        QSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLAT
                                                                                                                                                                                                                                                                                                                         Not really started.

Name-spinl; Synonyms-nrs;

Brachydanio rerio (Zebrafish) (Danio rerio).

Buachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.

NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryogenesis.";
Dev. Dyn. 223:298-305(2002).
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
ZFIN; ZDB-GENE-020228-1; spinl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.4%; Score 1266.5; DB 2; Length 506; Best Local Similarity 56.6%; Pred. No. 1.6e-69; Matches 252; Conservative 66; Mismatches 124; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21826209; PubMed=11836794;
Young R.M., Marty S., Nakano Y., Wang H., Yamamoto D., Lin S.,
Allende M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 AA; 54962 MW; 033B0DE912CC1ED2 CRC64;
                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub transporter.
Pfam; PF00083; Sugar_tr; 1.
PROSITE; PS50850; MFS; 1.
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                                                                                                                                                                              ALFFVSDRARAEQHLGERRAGVRVVHQRGP
                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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    344
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                             QSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLAT 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTK 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRGHADQ-LGDQLKARTSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 GLLGSAPFLFLALACARGSIVATYIFIFIGETLLSMNWAIVADILLYVVIFTRRSTAEAF 421
                                                      QIVLSHLIGDAGSPYLIGLISDRLRRSWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGT 481
                                                                                                                                                                                                                                                                                                                                                            2 AGSDTAPFLSQADDPDDGPAPGHPGLPGPMGNPKSGELEVPDCEGLQRITGLSRGHSTLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Gaps
                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
43.8%; Score 1278; DB 2; Length 528;
Best Local Similarity 52.2%; Pred. No. 3.2e-70;
Matches 266; Conservative 64; Mismatches 164; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 AA; 56860 MW; 85D4029B9B69827C CRC64;
                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                             528 AA
                                                                                  ALFFVSDRARAEQHLGERRAGVRVVHQRGP 552
                                                                                                 |:| || ||: |: | AMFIEDDRRRAQLHV----QGLLHESGP 505
                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-21238517; Pubmed=11340170;
                                                                                                                                                                                                                                          Spinster-like protein.
Name=2210013K02R1k;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
                                                                                                                                                                                                       (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 26,
                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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01-mar-2001
                              463
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01-JUN-2001
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    Query Match
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X STRAIN-BB; TISSUE-Whole booky;

X STRAIN-BB; TISSUE-Whole booky;

X STRAIN-BB; TISSUE-Whole E.A., Grouse L.H., Derge J.G.,

X STRAIN-BB; TISSUE-Whole E.A., Grouse L.H., Derge J.G.,

X Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Alusner R.D., Collins F.S., Moore T., Max S.I., Wang J., Halah F.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Warner A., Rubin G.M., Hong L.,

X Expleton M., Soares M.B., Bonaldo M.F., Carninoi F.,

X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

X Brows S.S., Loquellano N.A., Peters G.V., Abramson R.D., Mullahy S.J.,

Ruchards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Hichards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

X Hindlon D.K., Muzra M., Sodergren B.J., Lux, Gibbs R.A.,

X Hindlon D.K., Wazun A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

X Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

X Jones S.J., Marra M.A.,

X Green E.D., Marra M
                                                                                    466
                                                                                                                           412
                                                                                                                                                                                     347 OKTABICNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQRADPLVCAVGMLG
                       SAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALOSFT
                                                                                                          SHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPPVVVLGGMFFLATALFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
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Last annotation update)
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                                                                                                                                                                                                                                                                            527 VSDRARAEQHLGERRAGVRVVHQRG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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NCBI_TaxID=7955;
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SEQUENCE 506
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TISSUB-Mammary tumor metastatized to lung. Tumor arose spontaneously;

XTAINEZE2388257; PubMed=12477932;

XI Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XI Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XI Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

XI Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

XI Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XI Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XI Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.,

XI Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XI Raha S.S., Loquallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XI Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XI Ilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

XI Helton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XI Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

XI Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

XI Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                              S3 VLCYINLLNYMDRFTVAGVLPDIEHFFGIGDGTSGLLQTVFICSYMFLAPLFGYLGDRYN 112
                                                                                                                                                                                                                             406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AAPFLYLSIMPAQASTVATXVPIPLGETFLSMNWAIVADILLYVVIPTRRSTAEAFQIVL 412
                                                                                                                                                                                                  167 RKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAPTIIGDLFTKNT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                     233 GAIEAHPEHTLHRTSWLADMKALCRNPSFILSTFGFTAVAFVTGSLALWAPAFLFRAGVF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 SHLIGDAISPYLIGVVSDSIXES--NSYMWEPRSLQMSLLLCSPVAVAGGAFFLATAVFI 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 SAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAVALQSFT 466
                                                                                                                                                                                                                                                                                                                                   173 RINMLSIFYFAI PVGSGMGYIVGSKVDTVAKDWHWALRVTFGLGLLAVFLLMLVVQEPKR
                                                                                                                                                                                                                                                                                                                                                                                                        GHADQLGDQLKARTSWLRDMKALIRNRSYVFSSLATSAVSFATGALGMWIPLYLHRAQVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 OKTAETCNSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTORADPLVCAVGMLG
                                                                                                    107 ILSLGNVLNYLDRYTVAGVLLDIQQHFGVKDRGAGLLQSVPICSFMVAAPIFGYLGDRFN
                                                                                                                                                                                                                                                                                                      RTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGTLILILVPATKR
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                                                       Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                    <u>.</u>
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  Length 506;
43.3%; Score 1264.5; DB 2; Length 56.6%; Pred. No. 2.1e-69; ive 66; Mismatches 124; Indels
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 VSDRARAEQHLGERRAGVRVVHQRG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 EKDRDLAENYVPSDDAPI-VVPRSG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2210013K02Rik protein (Fragment).
Name=2210013K02Rik;
                          Best Local Similarity 56.6
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                       Similarity
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TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                          PIFGYLGDRFNRKVILSCGIFFWSAVTFSSSFIPQQYFWLLVLSRGLVGIGEASYSTIAP 215
                                                                                                                                                                                                                                                                                                                                                                    TIIGDLFTKNTRTLMLSVFYFAIPLGSGLGYITGSSVKQAAGDWHWALRVSPVLGMITGT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RADPLVCAVGMLGSAIFICLIFVAAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIP 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIPLYLHRAQVVQKTAETC-NSPPCGAKDSLIFGAITCFTGFLGVVTGAGATRWCRLKTQ 393
                                                                                                                                                                                                                                                                                                                          STAGESTORY N. 1

SUBMITTEE (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

RMBL, BC002297.1, -.

RMD, MG1:1920908; 2210013K02Rik.

GO, GO:0016021, C:Integral to membrane, IEA.

GO, GO:0016021, C:Integral to membrane, IEA.

GO, GO:0005315, F:transporter activity; IEA.

GO, GO:0006315, F:transporter activity; IEA.

RICEPTO; IPR000566; Lipocln_cytFABP.

RICEPTO; IPR007114; MFS.

RICEPTO; IRR005828; Sub_transporter.

REAM, PF00083; Sugar tr; 1.

REAM, PF00183; LIPOCALIN; UNKNOWN_1.
                                                       spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                 43.1%; Score 1258.5; DB 2; Length 486; 55.6%; Pred. No. 4.6e-69; ive 63; Mismatches 132; Indels 9;
                                                    TISSUE-Mammary tumor metastatized to lung. Tumor arose
                                                                                                                                                                                                                                            486 AA; 52571 MW; E924CA894E453B94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGMFFLATALFFVSDRARAEQHLGERRAGVRVVHQRGP 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 LGGAAFLGTAMFIEDDRRRAOLHV-----OGLLHESGP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPINL protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                             Best Local Similarity 55.6
Matches 255; Conservative
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                               SEQUENCE FROM N.A.
                                                                 Strausberg R.;
Submitted (JAN
                                                                                                                                                                                                                          Transmembrane.
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SEQUENCE
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Q86VU7
LD Q86VU
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DT 01-JU
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DT 01-JU
DT SPINL
OS HOMO
OC EUKAT
OC NAMMAMA
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,
Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhar N.K.,
A platchin S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nichards S., Worley R.C., Shevchenko Y., Bouffard G.G.,
Brakey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Myers R.M., Butterfield Y.S.,
Annes S.J., Marran M.A.,
Johns S.J., Marran M.A.,
Johns S.J., Marran M.A.,
Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.",
L. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Strausberg R.;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLUIAL ACATION: Integral membrane protein (By similarity).
EMBL; BC047741; AAH47741.1.1 -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0006151; F:transporter activity; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
Pfam: PF00083; Sugar_tr; 1.
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40.0%; Score 1167; DB 2; Length 476;
Best Local Similarity 49.4%; Pred. No. 1.8e-63;
Matches 254; Conservative 53; Mismatches 141; Indels 6
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MEDLINE=22388257; PubMed=12477932;
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RESULT 14
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                             371 IVLSHLLGDAGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGGAAFLGTA 430
464 SFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYALMLCPFVVVLGGMFFLATA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Bone; MEDLIRE=2049914; Pubmed=11042159; MEDLIRE=2049914; Pubmed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male bone cDNA, RIKEN full-length enriched library,
clone:9830002117 product:weakly similar to SPINSTER-LIKE PROTEIN.
Name=9830002117Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Bone;
C STRAIN=C57BL/6J; TISSUE=Bone;
A MEDLINE=2053013; Publed=11076861;
A MEDLINE=2053013; Publed=11076861;
A Mibate K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
A Conno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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STRAIN=CS7BL/6J; TISSUE=Bone;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J; TISSUE=Bone;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                    LFFVSDRARAEQHLGE--RRAGVR----VVHQRG 551
                                                                                                                                   :| :|| ||: |:
431 IFIEADRRRAQLHVQGLLHEAGSTDDRIVVPQRG 464
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Rad Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Rawai J., Kojima Y., Konno H., Koda M., Koya S., Kurihara C.,
Rad Matsuyama T., Miyazaki A., Nishin K., Numazaki R., Ohno M.,
Rad Sasaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Rad Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
Rad Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
Ramametau M., Hayashizaki Y.,
Rubited (Aug-2000) to the Embl./GenBank/DDBJ databases
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
REMIS, RACOS683; BAB12173: 11; -.
ROG GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0008215; Pranaporter activity; IEA.
BR InterPro: IPR00125; Prot in Serpin.
RICEPPRO: IPR00135; Sub_transporter.
BR RROSITE; PS00213; LIFOCALIN; UNKNOWN_1.
RROSITE; PS00213; LIFOCALIN; UNKNOWN_1.
RROSITE; PS00284; SERPIN; UNKNOWN_1.
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; Pred. No. 1e-61;
80; Mismatches 163; Indels
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                                                                                                                        [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE TO W.X., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T., Wan D.F., Gu J.R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPRO90114; MFS.
PROSITE: PSSO850; MFS; 1.
                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Novel human cDNA clones with function of inhibiting cancer cell
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      PRELIMINARY;
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                                                         Length 420;
                                                       Query Match
38.2%; Score 1115; DB 2; Length 4
Best Local Similarity 56.6%; Pred. No. 2.4e-60;
Matches 231; Conservative 50; Mismatches 119; Indels
EMBL; AF370423; AAQ15259.1; -. SFQUENCE 420 AA; 45301 MW; 5771BC5C252CD048 CRC64;
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Search completed: October 23, 2004, 13:14:07 Job time : 115 secs